STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 119718

TO: James Schultz
Location: rem/2d18/2c18
Art Unit: 1635
Monday, April 19, 2004

Case Serial Number: 10/024396

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
Phone: 571-272-2518 for B
assisted by Paul Schwartz
barbara.obryen@uspto.gov

Search Notes

Brian McCormack / Baker-Mackenzie
214-978-3007

SIRA Search and Information Resources Administration

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapm** and **.rapn**

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 19, 2004, 15:54:48 ; Search time 0.001 Seconds
(without alignments)
1.176 Million cell updates/sec

Title: US-10-024-396-3-COPY
Perfect score: 28
Sequence: 1 cgggccctacgtgtacagggagtccagg 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 21 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2000 summaries

Database : estdb:* EST

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	7.4	26.4	11	1	BM395068	ACCESSION:BM395068
	2	7	25.0	10	1	BM393918	ACCESSION:BM393918
	3	7	25.0	11	1	BM395068	ACCESSION:BM395068
c	4	6.4	22.9	10	1	BM393918	ACCESSION:BM393918

ALIGNMENTS

RESULT 1
BM395068/c
LOCUS BM395068 11 bp mRNA linear EST 17-JAN-2002
DEFINITION 50072-2-7-D04.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM395068
VERSION BM395068.1 GI:18195121
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 11)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .11
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 26.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 0;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 GGGCCCTAC 10
              |||||| ||
Db         11 GGGCCCGAC 3
```

RESULT 2
BM393918
LOCUS BM393918 10 bp mRNA linear EST 17-JAN-2002
DEFINITION 50072-2-11-H06.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM393918
VERSION BM393918.1 GI:18193971
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 10)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .10
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CGGGCCC 7
              |||||||
Db          2 CGGGCCC 8
```

RESULT 3
BM395068
LOCUS BM395068 11 bp mRNA linear EST 17-JAN-2002
DEFINITION 50072-2-7-D04.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM395068
VERSION BM395068.1 GI:18195121

```
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

  Query Match             25.0%;  Score 7;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCC 7
              |||||||
Db          5 CGGGCCC 11


RESULT 4
BM393918/c
LOCUS       BM393918                  10 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  50072-2-11-H06.r.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM393918
VERSION     BM393918.1  GI:18193971
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

  Query Match             22.9%;  Score 6.4;  DB 1;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 0;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GGGCCCTA 9
              |||||| |
Db          8 GGGCCCGA 1


Search completed: April 19, 2004, 15:54:48
Job time : 0.001 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 19, 2004, 14:25:24 ; Search time 0.001 Seconds
(without alignments)
208.040 Million cell updates/sec

Title: US-10-024-396-3-COPY
Perfect score: 28
Sequence: 1 cgggccctacgtgtacagggagtccagg 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 288 seqs, 3715 residues

Total number of hits satisfying chosen parameters: 576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 301 summaries

Database : rgedb:* GenEmbl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18.6	66.4	25	1	AX690109	ACCESSION:AX690109
	2	18.6	66.4	25	1	AX690110	ACCESSION:AX690110
	3	18.2	65.0	25	1	AX690107	ACCESSION:AX690107
	4	18.2	65.0	25	1	AX690108	ACCESSION:AX690108
	5	17.8	63.6	25	1	AX690105	ACCESSION:AX690105
	6	17.8	63.6	25	1	AX690106	ACCESSION:AX690106
	7	17.6	62.9	25	1	AX690111	ACCESSION:AX690111
	8	16.8	60.0	25	1	AX690104	ACCESSION:AX690104
	9	16.6	59.3	25	1	AX690112	ACCESSION:AX690112
	10	14.4	51.4	17	1	AX688603	ACCESSION:AX688603
	11	14.4	51.4	17	1	AX688604	ACCESSION:AX688604
	12	14.2	50.7	21	1	AR165205	ACCESSION:AR165205
	13	13.8	49.3	17	1	AX688605	ACCESSION:AX688605
	14	13.8	49.3	17	1	AX688606	ACCESSION:AX688606
	15	13.8	49.3	17	1	AX688607	ACCESSION:AX688607
	16	13.8	49.3	17	1	AX688608	ACCESSION:AX688608
	17	13.4	47.9	17	1	AX688602	ACCESSION:AX688602
c	18	13.4	47.9	18	1	AR058208	ACCESSION:AR058208
c	19	13.4	47.9	18	1	AR142361	ACCESSION:AR142361
c	20	13.4	47.9	20	1	AX449606	ACCESSION:AX449606
c	21	13.2	47.1	19	1	BD088466	ACCESSION:BD088466
c	22	13.2	47.1	19	1	AB069243	ACCESSION:AB069243
c	23	13.2	47.1	20	1	AX297476	ACCESSION:AX297476
	24	12.8	45.7	17	1	AX688609	ACCESSION:AX688609
	25	12.8	45.7	19	1	E32811	ACCESSION:E32811
	26	12.4	44.3	17	1	AX688601	ACCESSION:AX688601
c	27	12.4	44.3	18	1	AX711184	ACCESSION:AX711184
	28	12.4	44.3	19	1	AR016655	ACCESSION:AR016655
	29	12.4	44.3	19	1	AR110278	ACCESSION:AR110278
	30	12.2	43.6	17	1	AX419938	ACCESSION:AX419938
	31	12.2	43.6	17	1	AX688610	ACCESSION:AX688610
c	32	12.2	43.6	17	1	AX783828	ACCESSION:AX783828
c	33	12.2	43.6	17	1	AX783973	ACCESSION:AX783973
c	34	12.2	43.6	18	1	AR066781	ACCESSION:AR066781
	35	12.2	43.6	18	1	AR083092	ACCESSION:AR083092
	36	12	42.9	17	1	AX688599	ACCESSION:AX688599
	37	12	42.9	17	1	AX688600	ACCESSION:AX688600
	38	11.8	42.1	16	1	BD246816	ACCESSION:BD246816
	39	11.8	42.1	16	1	AX026612	ACCESSION:AX026612
c	40	11.4	40.7	17	1	AX711182	ACCESSION:AX711182
	41	11.2	40.0	16	1	AR001333	ACCESSION:AR001333
	42	11.2	40.0	16	1	AR037513	ACCESSION:AR037513
	43	11.2	40.0	16	1	AR062793	ACCESSION:AR062793
	44	11.2	40.0	16	1	AR087871	ACCESSION:AR087871
	45	11.2	40.0	16	1	AR091341	ACCESSION:AR091341
	46	11.2	40.0	16	1	AR118047	ACCESSION:AR118047
	47	11.2	40.0	16	1	AR127766	ACCESSION:AR127766
	48	11.2	40.0	16	1	AR144933	ACCESSION:AR144933
	49	11.2	40.0	16	1	AR145934	ACCESSION:AR145934
	50	11.2	40.0	16	1	I41167	ACCESSION:I41167
	51	11.2	40.0	17	1	BD259424	ACCESSION:BD259424
c	52	11.2	40.0	17	1	AX265559	ACCESSION:AX265559
	53	11.2	40.0	17	1	AX265560	ACCESSION:AX265560
	54	11.2	40.0	17	1	AX688611	ACCESSION:AX688611
c	55	11.2	40.0	17	1	AX783827	ACCESSION:AX783827
c	56	11.2	40.0	17	1	AX783829	ACCESSION:AX783829
c	57	11.2	40.0	17	1	AX783972	ACCESSION:AX783972
c	58	11.2	40.0	17	1	AX783974	ACCESSION:AX783974
	59	10.8	38.6	15	1	AR033355	ACCESSION:AR033355
	60	10.8	38.6	15	1	AR113177	ACCESSION:AR113177
	61	10.8	38.6	15	1	I57584	ACCESSION:I57584
c	62	10.8	38.6	15	1	AR180569	ACCESSION:AR180569
	63	10.8	38.6	15	1	BD207088	ACCESSION:BD207088
c	64	10	35.7	10	1	BD065320	ACCESSION:BD065320
c	65	10	35.7	11	1	AX470525	ACCESSION:AX470525
c	66	10	35.7	11	1	AX629206	ACCESSION:AX629206
	67	10	35.7	15	1	AR033531	ACCESSION:AR033531
	68	10	35.7	15	1	AR113353	ACCESSION:AR113353
	69	10	35.7	15	1	I38986	ACCESSION:I38986
	70	10	35.7	15	1	I57760	ACCESSION:I57760
	71	10	35.7	15	1	AX635280	ACCESSION:AX635280
	72	10	35.7	15	1	BD207264	ACCESSION:BD207264
	73	9.8	35.0	14	1	A42545	ACCESSION:A42545
	74	9.8	35.0	14	1	A88736	ACCESSION:A88736
c	75	9.8	35.0	14	1	AR253087	ACCESSION:AR253087
	76	9.8	35.0	14	1	BD066249	ACCESSION:BD066249
	77	9.8	35.0	15	1	AR033349	ACCESSION:AR033349
	78	9.8	35.0	15	1	AR113171	ACCESSION:AR113171
	79	9.8	35.0	15	1	BD263790	ACCESSION:BD263790
	80	9.8	35.0	15	1	I57578	ACCESSION:I57578
	81	9.8	35.0	15	1	AX048276	ACCESSION:AX048276
c	82	9.8	35.0	15	1	AX362585	ACCESSION:AX362585
	83	9.8	35.0	15	1	BD207082	ACCESSION:BD207082
c	84	9.4	33.6	11	1	AX625951	ACCESSION:AX625951
c	85	9.4	33.6	11	1	AX627912	ACCESSION:AX627912
c	86	9.4	33.6	11	1	AX628430	ACCESSION:AX628430
c	87	9.4	33.6	11	1	AX628528	ACCESSION:AX628528
	88	9.4	33.6	12	1	AR199211	ACCESSION:AR199211
	89	9.4	33.6	12	1	AR362486	ACCESSION:AR362486
c	90	9.4	33.6	12	1	AR362486	ACCESSION:AR362486
c	91	9.2	32.9	14	1	A42646	ACCESSION:A42646
c	92	9.2	32.9	14	1	A88835	ACCESSION:A88835
c	93	9.2	32.9	14	1	AR024070	ACCESSION:AR024070
c	94	9.2	32.9	14	1	AR224289	ACCESSION:AR224289
c	95	9.2	32.9	14	1	AX711052	ACCESSION:AX711052
c	96	9.2	32.9	14	1	BD001174	ACCESSION:BD001174
c	97	9.2	32.9	14	1	BD001603	ACCESSION:BD001603
c	98	9.2	32.9	14	1	BD066348	ACCESSION:BD066348
	99	9	32.1	10	1	AX152114	ACCESSION:AX152114
c	100	9	32.1	11	1	AX626581	ACCESSION:AX626581
c	101	9	32.1	11	1	AX628461	ACCESSION:AX628461
c	102	9	32.1	12	1	A47646	ACCESSION:A47646
c	103	9	32.1	12	1	AR027864	ACCESSION:AR027864
c	104	9	32.1	17	1	BD259424	ACCESSION:BD259424
c	105	8.8	31.4	12	1	AR199211	ACCESSION:AR199211
	106	8.8	31.4	12	1	A97287	ACCESSION:A97287

c	107	8.8	31.4	12	1	AR167847	ACCESSION:AR167847
c	108	8.8	31.4	12	1	E29731	ACCESSION:E29731
c	109	8.8	31.4	12	1	E38837	ACCESSION:E38837
c	110	8.8	31.4	12	1	E64263	ACCESSION:E64263
	111	8.8	31.4	13	1	AR407937	ACCESSION:AR407937
c	112	8.4	30.0	10	1	AR088591	ACCESSION:AR088591
c	113	8.4	30.0	10	1	AR099558	ACCESSION:AR099558
c	114	8.4	30.0	10	1	AR178839	ACCESSION:AR178839
c	115	8.4	30.0	10	1	E54652	ACCESSION:E54652
	116	8.4	30.0	10	1	AR336839	ACCESSION:AR336839
c	117	8.4	30.0	10	1	AX113024	ACCESSION:AX113024
c	118	8.4	30.0	10	1	AX153342	ACCESSION:AX153342
	119	8.4	30.0	10	1	AX377356	ACCESSION:AX377356
c	120	8.4	30.0	10	1	BD166783	ACCESSION:BD166783
c	121	8.4	30.0	10	1	BD167020	ACCESSION:BD167020
c	122	8.4	30.0	10	1	BD167059	ACCESSION:BD167059
c	123	8.4	30.0	10	1	BD167158	ACCESSION:BD167158
c	124	8.4	30.0	11	1	AR099559	ACCESSION:AR099559
c	125	8.4	30.0	11	1	AR178840	ACCESSION:AR178840
	126	8.4	30.0	11	1	BD241058	ACCESSION:BD241058
c	127	8.4	30.0	11	1	AR301464	ACCESSION:AR301464
	128	8.4	30.0	11	1	AX099043	ACCESSION:AX099043
c	129	8.4	30.0	11	1	AX099044	ACCESSION:AX099044
c	130	8.4	30.0	11	1	AX470626	ACCESSION:AX470626
	131	8.4	30.0	11	1	AX470645	ACCESSION:AX470645
	132	8.4	30.0	11	1	AX470757	ACCESSION:AX470757
	133	8.4	30.0	11	1	AX470853	ACCESSION:AX470853
c	134	8.4	30.0	11	1	AX471193	ACCESSION:AX471193
	135	8.4	30.0	11	1	AX472098	ACCESSION:AX472098
	136	8.4	30.0	11	1	AX623332	ACCESSION:AX623332
c	137	8.4	30.0	11	1	AX623370	ACCESSION:AX623370
c	138	8.4	30.0	11	1	AX623664	ACCESSION:AX623664
	139	8.4	30.0	11	1	AX623917	ACCESSION:AX623917
c	140	8.4	30.0	11	1	AX624031	ACCESSION:AX624031
	141	8.4	30.0	11	1	AX624952	ACCESSION:AX624952
c	142	8.4	30.0	11	1	AX625222	ACCESSION:AX625222
	143	8.4	30.0	11	1	AX625736	ACCESSION:AX625736
	144	8.4	30.0	11	1	AX627101	ACCESSION:AX627101
	145	8.4	30.0	11	1	AX629184	ACCESSION:AX629184
c	146	8.4	30.0	11	1	AX629283	ACCESSION:AX629283
c	147	8.4	30.0	11	1	AX629976	ACCESSION:AX629976
	148	8.4	30.0	11	1	AX630753	ACCESSION:AX630753
c	149	8.4	30.0	11	1	AX630791	ACCESSION:AX630791
c	150	8.4	30.0	11	1	AX631085	ACCESSION:AX631085
	151	8.4	30.0	11	1	AX631338	ACCESSION:AX631338
c	152	8.4	30.0	11	1	AX631452	ACCESSION:AX631452
	153	8.4	30.0	11	1	AX632373	ACCESSION:AX632373
c	154	8.4	30.0	11	1	AX632643	ACCESSION:AX632643
c	155	8.4	30.0	11	1	BD124214	ACCESSION:BD124214
c	156	8.4	30.0	12	1	A47668	ACCESSION:A47668
	157	8.4	30.0	12	1	AR024089	ACCESSION:AR024089
c	158	8.4	30.0	12	1	AR027886	ACCESSION:AR027886
c	159	8.4	30.0	12	1	AR099560	ACCESSION:AR099560
c	160	8.4	30.0	12	1	AR167743	ACCESSION:AR167743
	161	8.4	30.0	12	1	AR178738	ACCESSION:AR178738
c	162	8.4	30.0	12	1	AR178841	ACCESSION:AR178841
	163	8.4	30.0	12	1	BD251252	ACCESSION:BD251252
c	164	8.4	30.0	12	1	E29627	ACCESSION:E29627
c	165	8.4	30.0	12	1	E38733	ACCESSION:E38733
c	166	8.4	30.0	12	1	E64159	ACCESSION:E64159
	167	8.4	30.0	12	1	AR205443	ACCESSION:AR205443
	168	8.4	30.0	12	1	AR220135	ACCESSION:AR220135
	169	8.4	30.0	12	1	AR221524	ACCESSION:AR221524
	170	8.4	30.0	12	1	AR224308	ACCESSION:AR224308
	171	8.4	30.0	12	1	AR254226	ACCESSION:AR254226
	172	8.4	30.0	12	1	AR282432	ACCESSION:AR282432
	173	8.4	30.0	12	1	AR368339	ACCESSION:AR368339
c	174	8.4	30.0	12	1	AX463121	ACCESSION:AX463121
	175	8.4	30.0	12	1	AX711090	ACCESSION:AX711090
	176	8.4	30.0	12	1	BD001193	ACCESSION:BD001193
	177	8.4	30.0	12	1	BD001622	ACCESSION:BD001622
c	178	8.2	29.3	21	1	AR165205	ACCESSION:AR165205
c	179	8	28.6	9	1	AX456625	ACCESSION:AX456625
c	180	8	28.6	9	1	AX668649	ACCESSION:AX668649
c	181	8	28.6	9	1	AX668651	ACCESSION:AX668651
	182	8	28.6	9	1	AX668746	ACCESSION:AX668746
c	183	8	28.6	9	1	AX669004	ACCESSION:AX669004
c	184	8	28.6	9	1	AX669005	ACCESSION:AX669005
	185	8	28.6	10	1	A78814	ACCESSION:A78814
	186	8	28.6	10	1	BD238631	ACCESSION:BD238631
	187	8	28.6	10	1	BD240218	ACCESSION:BD240218
c	188	8	28.6	10	1	BD242821	ACCESSION:BD242821
	189	8	28.6	10	1	E54660	ACCESSION:E54660
	190	8	28.6	10	1	I63091	ACCESSION:I63091
c	191	8	28.6	10	1	AR274316	ACCESSION:AR274316
c	192	8	28.6	10	1	AX033036	ACCESSION:AX033036
	193	8	28.6	10	1	AX104933	ACCESSION:AX104933
c	194	8	28.6	10	1	AX152549	ACCESSION:AX152549
c	195	8	28.6	10	1	AX152759	ACCESSION:AX152759
c	196	8	28.6	10	1	AX153021	ACCESSION:AX153021
c	197	8	28.6	10	1	AX301658	ACCESSION:AX301658
	198	8	28.6	10	1	AX374632	ACCESSION:AX374632
	199	8	28.6	10	1	BD007893	ACCESSION:BD007893
c	200	8	28.6	10	1	BD007921	ACCESSION:BD007921
	201	8	28.6	10	1	BD065273	ACCESSION:BD065273
c	202	8	28.6	10	1	BD083323	ACCESSION:BD083323
	203	8	28.6	10	1	BD167068	ACCESSION:BD167068
	204	8	28.6	10	1	BD167170	ACCESSION:BD167170
	205	8	28.6	11	1	AR282864	ACCESSION:AR282864
	206	8	28.6	11	1	AX393110	ACCESSION:AX393110
	207	8	28.6	11	1	AX421267	ACCESSION:AX421267
c	208	8	28.6	11	1	AX421268	ACCESSION:AX421268
c	209	8	28.6	11	1	AX470469	ACCESSION:AX470469
	210	8	28.6	11	1	AX470788	ACCESSION:AX470788
c	211	8	28.6	11	1	AX470933	ACCESSION:AX470933
	212	8	28.6	11	1	AX471363	ACCESSION:AX471363
	213	8	28.6	11	1	AX471851	ACCESSION:AX471851
	214	8	28.6	11	1	AX623060	ACCESSION:AX623060
c	215	8	28.6	11	1	AX623555	ACCESSION:AX623555
	216	8	28.6	11	1	AX624143	ACCESSION:AX624143
c	217	8	28.6	11	1	AX625138	ACCESSION:AX625138
c	218	8	28.6	11	1	AX625188	ACCESSION:AX625188
	219	8	28.6	11	1	AX625450	ACCESSION:AX625450
c	220	8	28.6	11	1	AX625464	ACCESSION:AX625464
	221	8	28.6	11	1	AX625855	ACCESSION:AX625855
	222	8	28.6	11	1	AX626664	ACCESSION:AX626664
	223	8	28.6	11	1	AX627013	ACCESSION:AX627013
c	224	8	28.6	11	1	AX627782	ACCESSION:AX627782
c	225	8	28.6	11	1	AX629261	ACCESSION:AX629261
	226	8	28.6	11	1	AX629639	ACCESSION:AX629639
c	227	8	28.6	11	1	AX629743	ACCESSION:AX629743
	228	8	28.6	11	1	AX630481	ACCESSION:AX630481
c	229	8	28.6	11	1	AX630976	ACCESSION:AX630976
	230	8	28.6	11	1	AX631564	ACCESSION:AX631564
c	231	8	28.6	11	1	AX632559	ACCESSION:AX632559
c	232	8	28.6	11	1	AX632609	ACCESSION:AX632609
	233	8	28.6	11	1	AX632794	ACCESSION:AX632794
	234	8	28.6	12	1	I11566	ACCESSION:I11566
	235	8	28.6	12	1	I14185	ACCESSION:I14185
c	236	8	28.6	12	1	I24587	ACCESSION:I24587
	237	8	28.6	12	1	AX235321	ACCESSION:AX235321
	238	8	28.6	17	1	AX711182	ACCESSION:AX711182
	239	7.8	27.9	11	1	AX625951	ACCESSION:AX625951
c	240	7.8	27.9	11	1	AX472098	ACCESSION:AX472098
	241	7.8	27.9	11	1	I16095	ACCESSION:I16095
	242	7.8	27.9	11	1	AR301655	ACCESSION:AR301655
c	243	7.8	27.9	11	1	AR301691	ACCESSION:AR301691
c	244	7.8	27.9	11	1	AX470747	ACCESSION:AX470747
c	245	7.8	27.9	11	1	AX470906	ACCESSION:AX470906
c	246	7.8	27.9	11	1	AX470952	ACCESSION:AX470952
	247	7.8	27.9	11	1	AX471524	ACCESSION:AX471524
c	248	7.8	27.9	11	1	AX471669	ACCESSION:AX471669
c	249	7.8	27.9	11	1	AX471699	ACCESSION:AX471699
c	250	7.8	27.9	11	1	AX471796	ACCESSION:AX471796
c	251	7.8	27.9	11	1	AX623640	ACCESSION:AX623640
c	252	7.8	27.9	11	1	AX624024	ACCESSION:AX624024

c	253	7.8	27.9	11	1	AX624330 ACCESSION:AX624330
c	254	7.8	27.9	11	1	AX624837 ACCESSION:AX624837
c	255	7.8	27.9	11	1	AX625047 ACCESSION:AX625047
	256	7.8	27.9	11	1	AX625403 ACCESSION:AX625403
	257	7.8	27.9	11	1	AX625794 ACCESSION:AX625794
c	258	7.8	27.9	11	1	AX626034 ACCESSION:AX626034
c	259	7.8	27.9	11	1	AX626752 ACCESSION:AX626752
c	260	7.8	27.9	11	1	AX626783 ACCESSION:AX626783
	261	7.8	27.9	11	1	AX626888 ACCESSION:AX626888
	262	7.8	27.9	11	1	AX627660 ACCESSION:AX627660
	263	7.8	27.9	11	1	AX627965 ACCESSION:AX627965
c	264	7.8	27.9	11	1	AX628121 ACCESSION:AX628121
c	265	7.8	27.9	11	1	AX628521 ACCESSION:AX628521
c	266	7.8	27.9	11	1	AX628699 ACCESSION:AX628699
	267	7.8	27.9	11	1	AX629205 ACCESSION:AX629205
	268	7.8	27.9	11	1	AX629571 ACCESSION:AX629571
	269	7.8	27.9	11	1	AX629648 ACCESSION:AX629648
c	270	7.8	27.9	11	1	AX629882 ACCESSION:AX629882
	271	7.8	27.9	11	1	AX630279 ACCESSION:AX630279
c	272	7.8	27.9	11	1	AX631061 ACCESSION:AX631061
c	273	7.8	27.9	11	1	AX631445 ACCESSION:AX631445
c	274	7.8	27.9	11	1	AX631751 ACCESSION:AX631751
c	275	7.8	27.9	11	1	AX632258 ACCESSION:AX632258
c	276	7.8	27.9	11	1	AX632468 ACCESSION:AX632468
	277	7.8	27.9	11	1	BD124405 ACCESSION:BD124405
c	278	7.8	27.9	11	1	BD124441 ACCESSION:BD124441
c	279	7.8	27.9	12	1	A47665 ACCESSION:A47665
c	280	7.8	27.9	12	1	A91496 ACCESSION:A91496
c	281	7.8	27.9	12	1	AR027883 ACCESSION:AR027883
c	282	7.8	27.9	12	1	AR167661 ACCESSION:AR167661
c	283	7.8	27.9	12	1	E29545 ACCESSION:E29545
c	284	7.8	27.9	12	1	E38651 ACCESSION:E38651
c	285	7.8	27.9	12	1	E64077 ACCESSION:E64077
c	286	7.8	27.9	12	1	I23754 ACCESSION:I23754
c	287	7.8	27.9	12	1	I35021 ACCESSION:I35021
	288	7.8	27.9	12	1	AR224412 ACCESSION:AR224412
c	289	7.8	27.9	12	1	AX073604 ACCESSION:AX073604
c	290	7.8	27.9	12	1	AX073609 ACCESSION:AX073609
	291	7.8	27.9	12	1	AX105625 ACCESSION:AX105625
c	292	7.8	27.9	12	1	AX454105 ACCESSION:AX454105
c	293	7.8	27.9	12	1	AX454110 ACCESSION:AX454110
c	294	7.8	27.9	12	1	BD023278 ACCESSION:BD023278
c	295	7.8	27.9	25	1	AX690109 ACCESSION:AX690109
c	296	7.8	27.9	25	1	AX690110 ACCESSION:AX690110
c	297	7.8	27.9	25	1	AX690107 ACCESSION:AX690107
c	298	7.8	27.9	25	1	AX690108 ACCESSION:AX690108
c	299	7.8	27.9	25	1	AX690111 ACCESSION:AX690111
c	300	7.8	27.9	25	1	AX690112 ACCESSION:AX690112
c	301	7.6	27.1	10	1	AX096928 ACCESSION:AX096928

ALIGNMENTS

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RESULT 1
AX690109
LOCUS       AX690109                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 2841 from Patent EP1281758.
ACCESSION   AX690109
VERSION     AX690109.1  GI:29412967
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 2841 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             66.4%;  Score 18.6;  DB 1;  Length 25;
  Best Local Similarity   84.0%;  Pred. No. 2.5;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTACAGGGAGTCCAG 27
              |||||||||||| ||| |||| | |
Db          1 GGCCCTACGTGTGCAGCGAGTGCTG 25


RESULT 2
AX690110
LOCUS       AX690110                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 2842 from Patent EP1281758.
ACCESSION   AX690110
VERSION     AX690110.1  GI:29412968
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 2842 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             66.4%;  Score 18.6;  DB 1;  Length 25;
  Best Local Similarity   84.0%;  Pred. No. 2.5;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTACAGGGAGTCCAGG 28
              |||||||||||| ||| |||| | ||
Db          1 GCCCTACGTGTGCAGCGAGTGCTGG 25


RESULT 3
AX690107
LOCUS       AX690107                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 2839 from Patent EP1281758.
ACCESSION   AX690107
VERSION     AX690107.1  GI:29412965
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 2839 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             65.0%;  Score 18.2;  DB 1;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 3.1;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTACAGGGAGTCC 25
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                  ||||||||||||| ||| |||| |
Db          3 GGCCCTACGTGTGCAGCGAGTGC 25


RESULT 4
AX690108
LOCUS       AX690108                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 2840 from Patent EP1281758.
ACCESSION   AX690108
VERSION     AX690108.1  GI:29412966
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 2840 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"


  Query Match             65.0%;  Score 18.2;  DB 1;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 3.1;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTACAGGGAGTCC 25
              ||||||||||||| ||| |||| |
Db          2 GGCCCTACGTGTGCAGCGAGTGC 24


RESULT 5
AX690105
LOCUS       AX690105                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 2837 from Patent EP1281758.
ACCESSION   AX690105
VERSION     AX690105.1  GI:29412963
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 2837 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"


  Query Match             63.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 3.8;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTACAGGGAGT 23
              ||||||||||||| ||| ||||
Db          5 GGCCCTACGTGTGCAGCGAGT 25


RESULT 6
AX690106
LOCUS       AX690106                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 2838 from Patent EP1281758.
ACCESSION   AX690106
VERSION     AX690106.1  GI:29412964
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 2838 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"


  Query Match             63.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 3.8;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTACAGGGAGT 23
              ||||||||||||| ||| ||||
Db          4 GGCCCTACGTGTGCAGCGAGT 24


RESULT 7
AX690111
LOCUS       AX690111                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 2843 from Patent EP1281758.
ACCESSION   AX690111
VERSION     AX690111.1  GI:29412969
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 2843 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"


  Query Match             62.9%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 4.3;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTACAGGGAGTCCAGG 28
              |||||||||| ||| |||| | ||
Db          1 CCCTACGTGTGCAGCGAGTGCTGG 24


RESULT 8
AX690104
LOCUS       AX690104                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 2836 from Patent EP1281758.
ACCESSION   AX690104
VERSION     AX690104.1  GI:29412962
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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          mdz12
  JOURNAL   Patent: EP 1281758-A 2836 05-FEB-2003;
          Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             60.0%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 6.7;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTACAGGGAG 22
              |||||||||||| ||| |||
Db          6 GGCCCTACGTGTGCAGCGAG 25


RESULT 9
AX690112
LOCUS       AX690112                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 2844 from Patent EP1281758.
ACCESSION   AX690112
VERSION     AX690112.1  GI:29412970
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 2844 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             59.3%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 7.5;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACAGGGAGTCCAGG 28
              |||||||| ||| |||| | ||
Db          1 CCTACGTGTGCAGCGAGTGCTGG 23


RESULT 10
AX688603
LOCUS       AX688603                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 1335 from Patent EP1281758.
ACCESSION   AX688603
VERSION     AX688603.1  GI:29411305
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 1335 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             51.4%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 11;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTACAG 18
              ||||||||||||| |||
Db          2 GGCCCTACGTGTGCAG 17


RESULT 11
AX688604
LOCUS       AX688604                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 1336 from Patent EP1281758.
ACCESSION   AX688604
VERSION     AX688604.1  GI:29411306
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 1336 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             51.4%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 11;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTACAG 18
              ||||||||||||| |||
Db          1 GGCCCTACGTGTGCAG 16


RESULT 12
AR165205
LOCUS       AR165205                  21 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 19 from patent US 6274708.
ACCESSION   AR165205
VERSION     AR165205.1  GI:16238680
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Hilton,D.James.
  TITLE     Mouse interleukin-11 receptor
  JOURNAL   Patent: US 6274708-A 19 14-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             50.7%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 19;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCCAGG 28
              | |||||  ||||||||||
Db          3 CCTGTACTTGGAGTCCAGG 21


RESULT 13
AX688605
LOCUS       AX688605                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 1337 from Patent EP1281758.
```

```
ACCESSION   AX688605
VERSION     AX688605.1  GI:29411307
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 1337 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             49.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 15;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTACAGGG 20
              ||||||||||| ||| |
Db          1 GCCCTACGTGTGCAGCG 17


RESULT 14
AX688606
LOCUS       AX688606                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 1338 from Patent EP1281758.
ACCESSION   AX688606
VERSION     AX688606.1  GI:29411308
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 1338 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             49.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 15;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTACAGGGA 21
              ||||||||||| ||| ||
Db          1 CCCTACGTGTGCAGCGA 17


RESULT 15
AX688607
LOCUS       AX688607                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 1339 from Patent EP1281758.
ACCESSION   AX688607
VERSION     AX688607.1  GI:29411309
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 1339 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             49.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 15;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACAGGGAG 22
              ||||||||| ||| |||
Db          1 CCTACGTGTGCAGCGAG 17


RESULT 16
AX688608
LOCUS       AX688608                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 1340 from Patent EP1281758.
ACCESSION   AX688608
VERSION     AX688608.1  GI:29411310
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 1340 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             49.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 15;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGGGAGT 23
              ||||||||| ||| ||||
Db          1 CTACGTGTGCAGCGAGT 17


RESULT 17
AX688602
LOCUS       AX688602                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 1334 from Patent EP1281758.
ACCESSION   AX688602
VERSION     AX688602.1  GI:29411304
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 1334 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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  Query Match             47.9%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 19;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTACA 17
              ||||||||||||| ||
Db          3 GGCCCTACGTGTGCA 17


RESULT 18
AR058208/c
LOCUS       AR058208                 18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 6 from patent US 5837694.
ACCESSION   AR058208
VERSION     AR058208.1  GI:5983785
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Barrett,G.Leslie.
  TITLE     Method for enhancing neurone survival and agents useful for same
  JOURNAL   Patent: US 5837694-A 6 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             47.9%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 21;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGTCCA 26
              ||||||| |||||||
Db         17 TGTACAGCGAGTCCA 3


RESULT 19
AR142361/c
LOCUS       AR142361                 18 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 6 from patent US 6174869.
ACCESSION   AR142361
VERSION     AR142361.1  GI:15102661
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Barrett,G.Leslie.
  TITLE     Method for enhancing neurone survival and agents useful for same
  JOURNAL   Patent: US 6174869-A 6 16-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             47.9%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 21;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGTCCA 26
              ||||||| |||||||
Db         17 TGTACAGCGAGTCCA 3


RESULT 20
AX449606/c
LOCUS       AX449606                 20 bp    DNA     linear   PAT 03-JUL-2002
DEFINITION  Sequence 35 from Patent WO0210216.
ACCESSION   AX449606
VERSION     AX449606.1  GI:21698215
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Padigaru,M., Mezes,P., Mishra,V., Burgess,C., Casman,S.,
            Grosse,W.M., Alsobrook,J.P., Lepley,D.M., Gerlach,V.L.,
            Macdougall,J.R. and Smithson,G.
  TITLE     Proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 0210216-A 35 07-FEB-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primers"

  Query Match             47.9%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 27;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGTCCAGG 28
              || |||||||||||||
Db         17 TAGAGGGAGTCCAGG 3


RESULT 21
BD088466/c
LOCUS       BD088466                 19 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD088466
VERSION     BD088466.1  GI:22634076
KEYWORDS    JP 2001321190-A/710.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 710 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/710
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             47.1%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 27;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAGTCCAGG 28
              ||||| |||| | |||||
Db         19 GTGTAGAGGGTGGCCAGG 2


RESULT 22
AB069243/c
LOCUS       AB069243                 19 bp    DNA     linear   SYN 21-MAY-2003
DEFINITION  Synthetic construct DNA, reverse primer for human STS sts-L07033 at
```

```
            1p36.
ACCESSION   AB069243
VERSION     AB069243.1  GI:15130047
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
  TITLE     A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics 74 (1), 55-70 (2001)
  MEDLINE   21269192
   PUBMED   11374902
REFERENCE   2  (bases 1 to 19)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     misc_feature    1. .19
                     /note="reverse primer for human STS sts-L07033 at 1p36
                     sts-L07033 obtained from clones B7H21, B7I21, B135E5,
                     B196C16, B45G17, B62G22, B8D9, B173B2, B89K16, B213F1,
                     Human BAC library RPCI-11"

  Query Match             47.1%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 27;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          11 GTGTACAGGGAGTCCAGG 28
               ||||| |||| | |||||
Db          19 GTGTAGAGGGTGGCCAGG 2


RESULT 23
AX297476/c
LOCUS       AX297476                  20 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 9238 from Patent WO0179548.
ACCESSION   AX297476
VERSION     AX297476.1  GI:17059167
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
  TITLE     Method of designing addressable array for detection of nucleic acid
            sequence differences using ligase detection reaction
  JOURNAL   Patent: WO 0179548-A 9238 25-OCT-2001;
            CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Hypothetical Probe Sequence"

  Query Match             47.1%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 30;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          10 CGTGTACAGGGAGTCCAG 27
               |||||  |||||||||  |
Db          20 CGTGTGTAGGGAGTCCGG 3


RESULT 24
AX688609
LOCUS       AX688609                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 1341 from Patent EP1281758.
ACCESSION   AX688609
VERSION     AX688609.1  GI:29411311
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 1341 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             45.7%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 26;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGGGAGT 23
              ||||||| ||| ||||
Db          1 TACGTGTGCAGCGAGT 16


RESULT 25
E32811
LOCUS       E32811                    19 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Primer DNA and method for detecting mRNA encoding prostate
            gland-specific antigen by using the same.
ACCESSION   E32811
VERSION     E32811.1  GI:18623941
KEYWORDS    JP 2000069969-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Nakagawara,H.
  TITLE     Primer DNA and method for detecting mRNA encoding prostate
            gland-specific antigen by using the same
  JOURNAL   Patent: JP 2000069969-A 4 07-MAR-2000;
            HITACHI CHEMICAL CO LTD,KK NIHON IDENSHI KENKYUJO
COMMENT     OS   Unidentified
            PN   JP 2000069969-A/4
            PD   07-MAR-2000
            PF   28-AUG-1998 JP 1998243419
            PR
            PI   HIROKAZU NAKAGAWARA
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             45.7%;  Score 12.8;  DB 1;  Length 19;
  Best Local Similarity   87.5%;  Pred. No. 33;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy          6 CCTACGTGTACAGGGA 21
              |||  ||||||||||
Db          4 CCTTGGTGTACAGGGA 19


RESULT 26
AX688601
LOCUS       AX688601                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 1333 from Patent EP1281758.
ACCESSION   AX688601
VERSION     AX688601.1  GI:29411303
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 1333 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            44.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 32;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTAC 16
              |||||||||||| |
Db          4 GGCCCTACGTGTGC 17


RESULT 27
AX711184/c
LOCUS       AX711184                 18 bp    DNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 484 from Patent EP1288296.
ACCESSION   AX711184
VERSION     AX711184.1  GI:29787565
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 484 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic acid clone fragments"

  Query Match            44.3%;  Score 12.4;  DB 1;  Length 18;
  Best Local Similarity   92.9%;  Pred. No. 36;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCTACGTGT 14
              ||||||| ||||||
Db         14 CGGGCCCGACGTGT 1


RESULT 28
AR016655
LOCUS       AR016655                 19 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 18 from patent US 5776762.
ACCESSION   AR016655
VERSION     AR016655.1  GI:3972932
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   North,M., Nishina,P., Noben-Trauth,K. and Naggert,J.
  TITLE     Obesity associated genes
  JOURNAL   Patent: US 5776762-A 18 07-JUL-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match            44.3%;  Score 12.4;  DB 1;  Length 19;
  Best Local Similarity   92.9%;  Pred. No. 41;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAGTCCAGG 28
              |||||||| |||||
Db          6 ACAGGGAGACCAGG 19


RESULT 29
AR110278
LOCUS       AR110278                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 30 from patent US 6114502.
ACCESSION   AR110278
VERSION     AR110278.1  GI:12826554
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   North,M., Nishina,P., Naggert,J. and Noben-Trauth,K.
  TITLE     Gene family associated with neurosensory defects
  JOURNAL   Patent: US 6114502-A 30 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match            44.3%;  Score 12.4;  DB 1;  Length 19;
  Best Local Similarity   92.9%;  Pred. No. 41;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAGTCCAGG 28
              |||||||| |||||
Db          6 ACAGGGAGACCAGG 19


RESULT 30
AX419938
LOCUS       AX419938                 17 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 275 from Patent WO0198537.
ACCESSION   AX419938
VERSION     AX419938.1  GI:21524305
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lyamichev,V., Allawi,H., Dong,F., Neri,B.P. and Vener,I.T.
  TITLE     Nucleic acid accessible hybridization sites
  JOURNAL   Patent: WO 0198537-A 275 27-DEC-2001;
            THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
```

```
  Query Match             43.6%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 36;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 GGGCCCTACGTGTACAG 18
              || ||||| || |||||
Db          1 GGACCCTATGTCTACAG 17


RESULT 31
AX688610
LOCUS       AX688610                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 1342 from Patent EP1281758.
ACCESSION   AX688610
VERSION     AX688610.1  GI:29411312
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 1342 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             43.6%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 36;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          9 ACGTGTACAGGGAGTCC 25
              |||||| ||| |||| |
Db          1 ACGTGTGCAGCGAGTGC 17


RESULT 32
AX783828/c
LOCUS       AX783828                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Sequence 2159 from Patent WO03050284.
ACCESSION   AX783828
VERSION     AX783828.1  GI:32951677
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Guo,J.
  TITLE     Human prostate cancer candidate protein 1
  JOURNAL   Patent: WO 03050284-A 2159 19-JUN-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             43.6%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 36;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGTCCAGG 28
              || | |||||||| |||
Db         17 TGAAAAGGGAGTCAAGG 1


RESULT 33
AX783973/c
LOCUS       AX783973                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Sequence 2304 from Patent WO03050284.
ACCESSION   AX783973
VERSION     AX783973.1  GI:32951822
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Guo,J.
  TITLE     Human prostate cancer candidate protein 1
  JOURNAL   Patent: WO 03050284-A 2304 19-JUN-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             43.6%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 36;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTACAGGGA 21
              |||||||| || || ||
Db         17 CCCTACGTATAAAGAGA 1


RESULT 34
AR066781/c
LOCUS       AR066781                  18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 129 from patent US 5851760.
ACCESSION   AR066781
VERSION     AR066781.1  GI:5998003
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Evans,G.A. and Smith,M.W.
  TITLE     Method for generation of sequence sampled maps of complex genomes
  JOURNAL   Patent: US 5851760-A 129 22-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             43.6%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 41;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAGTCCAG 27
              ||| | |||||||||| |
Db         18 GTGGAAAGGGAGTCCGG 2


RESULT 35
AR083092
LOCUS       AR083092                  18 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 6 from patent US 5976803.
ACCESSION   AR083092
VERSION     AR083092.1  GI:10009882
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Meek,K.D.
  TITLE     Genetic test for equine severe combined immunodeficiency disease
  JOURNAL   Patent: US 5976803-A 6 02-NOV-1999;
```

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FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match            43.6%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 41;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGTCCAGG 28
              | |||||||| | ||||
Db          1 TCTACAGGGAATTCAGG 17


RESULT 36
AX688599
LOCUS       AX688599                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 1331 from Patent EP1281758.
ACCESSION   AX688599
VERSION     AX688599.1  GI:29411301
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 1331 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            42.9%;  Score 12;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGT 14
              ||||||||||||
Db          6 GGCCCTACGTGT 17


RESULT 37
AX688600
LOCUS       AX688600                 17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 1332 from Patent EP1281758.
ACCESSION   AX688600
VERSION     AX688600.1  GI:29411302
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 1332 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            42.9%;  Score 12;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGT 14
              ||||||||||||
Db          5 GGCCCTACGTGT 16


RESULT 38
BD246816
LOCUS       BD246816                 16 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Genotyping cytochrome expression.
ACCESSION   BD246816
VERSION     BD246816.1  GI:33056586
KEYWORDS    JP 2002533136-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Paulussen,A.D.C. and Armstrong,M.
  TITLE     Genotyping cytochrome expression
  JOURNAL   Patent: JP 2002533136-A 2 08-OCT-2002;
            JANSSEN PHARMACEUTICA NV
COMMENT     OS   Artificial Sequence
            PN   JP 2002533136-A/2
            PD   08-OCT-2002
            PF   22-DEC-1999 JP 2000591220
            PR   23-DEC-1998 GB    9828619.8
            PI   AIMEE DYMPHNE CATHERINE PAULUSSEN,MARTIN ARMSTRONG PC
            C12N15/09,C12Q1/02,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC
            Description of Artificial Sequence:primer
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match            42.1%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 39;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAGTCCAG 27
              |||||||||  |||
Db          2 GTACAGGGAGCACAG 16


RESULT 39
AX026612
LOCUS       AX026612                 16 bp    DNA     linear   PAT 16-SEP-2000
DEFINITION  Sequence 2 from Patent WO0039332.
ACCESSION   AX026612
VERSION     AX026612.1  GI:10187786
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Paulussen,A.D. and Armstrong,M.
  TITLE     Genotyping cytochrome expression
  JOURNAL   Patent: WO 0039332-A 2 06-JUL-2000;
            JANSSEN PHARMACEUTICA NV (BE) ; PAULUSSEN AIMEE DYMPHNE CATHER (BE)
            ; ARMSTRONG MARTIN (GB)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer"

  Query Match            42.1%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 39;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy          13 GTACAGGGAGTCCAG 27
               ||||||||||  |||
Db           2 GTACAGGGAGCACAG 16


RESULT 40
AX711182/c
LOCUS       AX711182                 17 bp    DNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 482 from Patent EP1288296.
ACCESSION   AX711182
VERSION     AX711182.1  GI:29787563
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 482 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic acid clone fragments"

  Query Match             40.7%;  Score 11.4;  DB 1;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 55;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           2 GGGCCCTACGTGT 14
               ||||||  ||||||
Db          13 GGGCCCGACGTGT 1


RESULT 41
AR001333
LOCUS       AR001333                 16 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 23 from patent US 5739027.
ACCESSION   AR001333
VERSION     AR001333.1  GI:3963400
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kamb,A.
  TITLE     MTS1E1.beta. gene
  JOURNAL   Patent: US 5739027-A 23 14-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 54;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          10 CGTGTACAGGGAGTCC 25
               |||||  ||||  || ||
Db           1 CGTGTCCAGGAAGCCC 16


RESULT 42
AR037513
LOCUS       AR037513                 16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 23 from patent US 5801236.
ACCESSION   AR037513
VERSION     AR037513.1  GI:5955369
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kamb,A.
  TITLE     Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes
  JOURNAL   Patent: US 5801236-A 23 01-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 54;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          10 CGTGTACAGGGAGTCC 25
               |||||  ||||  || ||
Db           1 CGTGTCCAGGAAGCCC 16


RESULT 43
AR062793
LOCUS       AR062793                 16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 23 from patent US 5843756.
ACCESSION   AR062793
VERSION     AR062793.1  GI:5990484
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Stone,S., Jiang,P. and Kamb,A.
  TITLE     Mouse MTSI gene
  JOURNAL   Patent: US 5843756-A 23 01-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 54;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          10 CGTGTACAGGGAGTCC 25
               |||||  ||||  || ||
Db           1 CGTGTCCAGGAAGCCC 16


RESULT 44
AR087871
LOCUS       AR087871                 16 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 23 from patent US 5989815.
ACCESSION   AR087871
VERSION     AR087871.1  GI:10014634
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.
  TITLE     Methods for detecting predisposition to cancer at the MTS gene
  JOURNAL   Patent: US 5989815-A 23 23-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 54;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          10 CGTGTACAGGGAGTCC 25
               |||||  ||||  || ||
```

```
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 45
AR091341
LOCUS       AR091341                  16 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 23 from patent US 5994095.
ACCESSION   AR091341
VERSION     AR091341.1  GI:10018096
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kamb,A.
  TITLE     MTS2 gene
  JOURNAL   Patent: US 5994095-A 23 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match           40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 54;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
              ||||| |||| || ||
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 46
AR118047
LOCUS       AR118047                  16 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 23 from patent US 6140473.
ACCESSION   AR118047
VERSION     AR118047.1  GI:14098953
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kamb,A.
  TITLE     Antibodies specific for MTS2 Polypeptide
  JOURNAL   Patent: US 6140473-A 23 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match           40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 54;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
              ||||| |||| || ||
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 47
AR127766
LOCUS       AR127766                  16 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 23 from patent US 6180776.
ACCESSION   AR127766
VERSION     AR127766.1  GI:14114361
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kamb,A.
  TITLE     MTS2 gene
  JOURNAL   Patent: US 6180776-A 23 30-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match           40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 54;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
              ||||| |||| || ||
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 48
AR144933
LOCUS       AR144933                  16 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 23 from patent US 6210949.
ACCESSION   AR144933
VERSION     AR144933.1  GI:15106800
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Stone,S., Jiang,P. and Kamb,A.
  TITLE     Mouse MTS2 gene
  JOURNAL   Patent: US 6210949-A 23 03-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match           40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 54;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
              ||||| |||| || ||
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 49
AR145934
LOCUS       AR145934                  16 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 23 from patent US 6218146.
ACCESSION   AR145934
VERSION     AR145934.1  GI:15109123
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kamb,A.
  TITLE     MTS2 gene
  JOURNAL   Patent: US 6218146-A 23 17-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match           40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 54;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
              ||||| |||| || ||
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 50
I41167
LOCUS       I41167                    16 bp    DNA     linear   PAT 13-MAY-1997
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```
DEFINITION  Sequence 23 from patent US 5624819.
ACCESSION   I41167
VERSION     I41167.1  GI:2081757
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.
  TITLE     Germline mutations in the MTS gene
  JOURNAL   Patent: US 5624819-A 23 29-APR-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 54;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
              ||||| |||| || ||
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 51
BD259424
LOCUS       BD259424                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD259424
VERSION     BD259424.1  GI:33069194
KEYWORDS    JP 2002541795-A/7217.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 7217 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/7217
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 61;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGGGAG 22
              |||| ||||| ||||
Db          1 CTACATGTACCAGGAG 16


RESULT 52
AX265559/c
LOCUS       AX265559                  17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 2950 from Patent WO0173002.
ACCESSION   AX265559
VERSION     AX265559.1  GI:16514358
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 2950 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 61;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          9 ACGTGTACAGGGAGTC 24
              || ||| ||||||| |
Db         17 ACTTGTCCAGGGAGGC 2


RESULT 53
AX265560
LOCUS       AX265560                  17 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 2951 from Patent WO0173002.
ACCESSION   AX265560
VERSION     AX265560.1  GI:16514359
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kmiec,E.B., Gamper,H.B. and Rice,M.C.
  TITLE     Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
  JOURNAL   Patent: WO 0173002-A 2951 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 61;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          9 ACGTGTACAGGGAGTC 24
              || ||| ||||||| |
Db          1 ACTTGTCCAGGGAGGC 16


RESULT 54
AX688611
LOCUS       AX688611                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 1343 from Patent EP1281758.
ACCESSION   AX688611
VERSION     AX688611.1  GI:29411313
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
```

```
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 1343 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 61;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
              ||||| ||| |||| |
Db          1 CGTGTGCAGCGAGTGC 16


RESULT 55
AX783827/c
LOCUS       AX783827                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Sequence 2158 from Patent WO03050284.
ACCESSION   AX783827
VERSION     AX783827.1  GI:32951676
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Guo,J.
  TITLE     Human prostate cancer candidate protein 1
  JOURNAL   Patent: WO 03050284-A 2158 19-JUN-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 61;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAGTCCAGG 28
              | | |||||||| |||
Db         17 GAAAAGGGAGTCAAGG 2


RESULT 56
AX783829/c
LOCUS       AX783829                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Sequence 2160 from Patent WO03050284.
ACCESSION   AX783829
VERSION     AX783829.1  GI:32951678
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Guo,J.
  TITLE     Human prostate cancer candidate protein 1
  JOURNAL   Patent: WO 03050284-A 2160 19-JUN-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 61;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGTCCAG 27
              || | |||||||| ||
Db         16 TGAAAAGGGAGTCAAG 1


RESULT 57
AX783972/c
LOCUS       AX783972                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Sequence 2303 from Patent WO03050284.
ACCESSION   AX783972
VERSION     AX783972.1  GI:32951821
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Guo,J.
  TITLE     Human prostate cancer candidate protein 1
  JOURNAL   Patent: WO 03050284-A 2303 19-JUN-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 61;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACAGGGA 21
              ||||||| || || ||
Db         17 CCTACGTATAAAGAGA 2


RESULT 58
AX783974/c
LOCUS       AX783974                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Sequence 2305 from Patent WO03050284.
ACCESSION   AX783974
VERSION     AX783974.1  GI:32951823
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Guo,J.
  TITLE     Human prostate cancer candidate protein 1
  JOURNAL   Patent: WO 03050284-A 2305 19-JUN-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES              Location/Qualifiers
     source           1. .17
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 61;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTACAGGG 20
              |||||||| || || |
Db         16 CCCTACGTATAAAGAG 1
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RESULT 59
AR033355
LOCUS       AR033355                  15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 121 from patent US 5869253.
ACCESSION   AR033355
VERSION     AR033355.1  GI:5948960
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Draper,K.G.
  TITLE     Method and reagent for inhibiting hepatitis C virus replication
  JOURNAL   Patent: US 5869253-A 121 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             38.6%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 58;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GGGCCCTACGTGTA 15
              ||||||| |||| |
Db          1 GGGCCCTCCGTGCA 14


RESULT 60
AR113177
LOCUS       AR113177                  15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 121 from patent US 6132966.
ACCESSION   AR113177
VERSION     AR113177.1  GI:14093499
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Draper,K.G.
  TITLE     Method and reagent for inhibiting hepatitis C virus replication
  JOURNAL   Patent: US 6132966-A 121 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             38.6%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 58;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GGGCCCTACGTGTA 15
              ||||||| |||| |
Db          1 GGGCCCTCCGTGCA 14


RESULT 61
I57584
LOCUS       I57584                    15 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 121 from patent US 5610054.
ACCESSION   I57584
VERSION     I57584.1  GI:2482648
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Draper,K.G.
  TITLE     Enzymatic RNA molecule targeted against Hepatitis C virus
  JOURNAL   Patent: US 5610054-A 121 11-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             38.6%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 58;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GGGCCCTACGTGTA 15
              ||||||| |||| |
Db          1 GGGCCCTCCGTGCA 14


RESULT 62
AR180569/c
LOCUS       AR180569                  15 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 637 from patent US 6333152.
ACCESSION   AR180569
VERSION     AR180569.1  GI:20222602
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
  TITLE     Gene expression profiles in normal and cancer cells
  JOURNAL   Patent: US 6333152-A 637 25-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             38.6%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 58;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAGTCCAGG 28
              |||| |||||||| |
Db         14 ACAGAGAGTCCATG 1


RESULT 63
BD207088
LOCUS       BD207088                  15 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION   BD207088
VERSION     BD207088.1  GI:33016858
KEYWORDS    JP 2002512791-A/678.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
  JOURNAL   Patent: JP 2002512791-A 678 08-MAY-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Hepatitis virus (hepatitis C virus)
            PN   JP 2002512791-A/678
            PD   08-MAY-2002
            PF   26-APR-1999 JP 2000545991
            PR   27-APR-1998 US    60/083217,18-SEP-1998 US    60/100842 PR
            25-FEB-1999 US    09/257608,23-MAR-1999 US    09/274553 PI
            LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A  PI
            PAVCO,
            PI   DENNIS MACEJAK
            PC   C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
            PC   A61K37/66,
            PC   C12N15/00
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   hepatitis C virus infection.
            FH   Key             Location/Qualifiers
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            FT   source          1. .15
            FT                   /organism='Hepatitis virus (hepatitis C  FT
                              virus)'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"

  Query Match             38.6%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 58;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GGGCCCTACGTGTA 15
              ||||||| |||| |
Db          1 GGGCCCTCCGTGCA 14


RESULT 64
BD065320/c
LOCUS       BD065320                 10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Characterization of the yeast transcriptome.
ACCESSION   BD065320
VERSION     BD065320.1  GI:22610923
KEYWORDS    JP 2001509017-A/256.
SOURCE      Saccharomyces cerevisiae (baker's yeast)
  ORGANISM  Saccharomyces cerevisiae
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Characterization of the yeast transcriptome
  JOURNAL   Patent: JP 2001509017-A 256 10-JUL-2001;
            THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT     OS   Saccharomyces cerevisiae (yeast)
            PN   JP 2001509017-A/256
            PD   10-JUL-2001
            PF   22-JAN-1998 JP 1998532117
            PR   23-JAN-1997 US    60/035917
            PI   VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
            C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
            Characterization of the yeast transcriptome
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Saccharomyces cerevisiae (yeast)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Saccharomyces cerevisiae"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4932"

  Query Match             35.7%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGT 23
              ||||||||||
Db         10 TACAGGGAGT 1


RESULT 65
AX470525/c
LOCUS       AX470525                 11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 102 from Patent WO02053773.
ACCESSION   AX470525
VERSION     AX470525.1  GI:22205650
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 102 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             35.7%;  Score 10;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGA 21
              ||||||||||
Db         10 TGTACAGGGA 1


RESULT 66
AX629206/c
LOCUS       AX629206                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6247 from Patent WO02053774.
ACCESSION   AX629206
VERSION     AX629206.1  GI:28457244
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6247 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             35.7%;  Score 10;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGA 21
              ||||||||||
Db         10 TGTACAGGGA 1


RESULT 67
AR033531
LOCUS       AR033531                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 297 from patent US 5869253.
ACCESSION   AR033531
VERSION     AR033531.1  GI:5949136
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Draper,K.G.
  TITLE     Method and reagent for inhibiting hepatitis C virus replication
  JOURNAL   Patent: US 5869253-A 297 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             35.7%;  Score 10;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCAGG 28
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              ||||||||||
Db          3 GGAGTCCAGG 12


RESULT 68
AR113353
LOCUS       AR113353                  15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 297 from patent US 6132966.
ACCESSION   AR113353
VERSION     AR113353.1  GI:14093675
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Draper,K.G.
  TITLE     Method and reagent for inhibiting hepatitis C virus replication
  JOURNAL   Patent: US 6132966-A 297 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             35.7%;  Score 10;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCAGG 28
              ||||||||||
Db          3 GGAGTCCAGG 12


RESULT 69
I38986
LOCUS       I38986                    15 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 24 from patent US 5616488.
ACCESSION   I38986
VERSION     I38986.1  GI:2083466
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
  TITLE     IL-5 targeted ribozymes
  JOURNAL   Patent: US 5616488-A 24 01-APR-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             35.7%;  Score 10;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTA 15
              ||||||||||
Db          5 CCTACGTGTA 14


RESULT 70
I57760
LOCUS       I57760                    15 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 297 from patent US 5610054.
ACCESSION   I57760
VERSION     I57760.1  GI:2482824
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Draper,K.G.
  TITLE     Enzymatic RNA molecule targeted against Hepatitis C virus
  JOURNAL   Patent: US 5610054-A 297 11-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             35.7%;  Score 10;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCAGG 28
              ||||||||||
Db          3 GGAGTCCAGG 12


RESULT 71
AX635280
LOCUS       AX635280                  15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2419 from Patent EP1260586.
ACCESSION   AX635280
VERSION     AX635280.1  GI:28470894
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 2419 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"

  Query Match             35.7%;  Score 10;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTA 15
              ||||||||||
Db          5 CCTACGTGTA 14


RESULT 72
BD207264
LOCUS       BD207264                  15 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION   BD207264
VERSION     BD207264.1  GI:33017034
KEYWORDS    JP 2002512791-A/854.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
  JOURNAL   Patent: JP 2002512791-A 854 08-MAY-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Hepatitis virus (hepatitis C virus)
            PN   JP 2002512791-A/854
            PD   08-MAY-2002
            PF   26-APR-1999 JP 2000545991
            PR   27-APR-1998 US    60/083217,18-SEP-1998 US    60/100842 PR
            25-FEB-1999 US    09/257608,23-MAR-1999 US    09/274553 PI
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            LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A  PI
            PAVCO,
            PI   DENNIS MACEJAK
            PC   C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
            PC   A61K37/66,
            PC   C12N15/00
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                       related to
            CC   hepatitis C virus infection.
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Hepatitis virus (hepatitis C  FT
                           virus)'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"

  Query Match             35.7%;  Score 10;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          19 GGAGTCCAGG 28
               ||||||||||
Db           3 GGAGTCCAGG 12


RESULT 73
A42545
LOCUS       A42545                    14 bp    DNA     linear   PAT 06-MAR-1997
DEFINITION  Sequence 61 from Patent WO9502051.
ACCESSION   A42545
VERSION     A42545.1  GI:2297994
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Schlingensiepen,G., Schlingensiepen,R., Schlingensiepen,K. and
            Brysch,W.
  TITLE     A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR
            PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND
            CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS
  JOURNAL   Patent: WO 9502051-A 61 19-JAN-1995;
            BIOGNOSTIK GES FUER BIOMOLEKUL (DE)
COMMENT     Other publication AU 7345694 950206.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 14;
  Best Local Similarity   84.6%;  Pred. No. 85;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          10 CGTGTACAGGGAG 22
               |||||| || |||
Db           2 CGTGTAGAGAGAG 14


RESULT 74
A88736
LOCUS       A88736                    14 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 884 from Patent WO9833904.
ACCESSION   A88736
VERSION     A88736.1  GI:6737306
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 884 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 14;
  Best Local Similarity   84.6%;  Pred. No. 85;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          10 CGTGTACAGGGAG 22
               |||||| || |||
Db           2 CGTGTAGAGAGAG 14


RESULT 75
AR253087/c
LOCUS       AR253087                  14 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 38 from patent US 6479242.
ACCESSION   AR253087
VERSION     AR253087.1  GI:27301448
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Guo,B. and Sun,X.
  TITLE     Method for genotyping of single nucleotide polymorphism
  JOURNAL   Patent: US 6479242-A 38 12-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 14;
  Best Local Similarity   84.6%;  Pred. No. 85;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAGTC 24
               ||  |||||||||
Db          14 TGGGCAGGGAGTC 2


RESULT 76
BD066249
LOCUS       BD066249                  14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD066249
VERSION     BD066249.1  GI:22611852
KEYWORDS    JP 2001511000-A/884.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 884 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/884
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                 Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Unknown'.
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FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 14;
  Best Local Similarity   84.6%;  Pred. No. 85;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAG 22
              |||||| || |||
Db          2 CGTGTAGAGAGAG 14


RESULT 77
AR033349
LOCUS       AR033349                 15 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 115 from patent US 5869253.
ACCESSION   AR033349
VERSION     AR033349.1  GI:5948954
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Draper,K.G.
  TITLE     Method and reagent for inhibiting hepatitis C virus replication
  JOURNAL   Patent: US 5869253-A 115 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 97;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTA 15
              | |||||||| ||
Db          2 GCCCCTACGTATA 14


RESULT 78
AR113171
LOCUS       AR113171                 15 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 115 from patent US 6132966.
ACCESSION   AR113171
VERSION     AR113171.1  GI:14093493
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Draper,K.G.
  TITLE     Method and reagent for inhibiting hepatitis C virus replication
  JOURNAL   Patent: US 6132966-A 115 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 97;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTA 15
              | |||||||| ||
Db          2 GCCCCTACGTATA 14


RESULT 79
BD263790
```

```
LOCUS       BD263790                 15 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Adeno-associated virus-delivered ribozyme compositions and methods
            of use.
ACCESSION   BD263790
VERSION     BD263790.1  GI:33073558
KEYWORDS    JP 2002542805-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and
            Burger,C.
  TITLE     Adeno-associated virus-delivered ribozyme compositions and methods
            of use
  JOURNAL   Patent: JP 2002542805-A 12 17-DEC-2002;
            UNIVERSITY OF FLORIDA
COMMENT     OS   Artificial Sequence
            PN   JP 2002542805-A/12
            PD   17-DEC-2002
            PF   28-APR-2000 JP 2000615402
            PR   30-APR-1999 US    60/131942
            PI   ALFRED S LEWIN,NICHOLAS MUZYCZKA,WILLIAM W HAUSWIRTH PI
            ,CHRISTIAN TESCHENDORF,
            PI   CORINNA BURGER
            PC   C12N15/09,A01K67/027,C12N9/00,C12Q1/68,C12N15/00 CC
            Description of Artificial Sequence: SYNTHETIC PEPTIDE FH   Key
                  Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 97;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCCAGG 28
              |||  ||||||||
Db          1 CAGACAGTCCAGG 13


RESULT 80
I57578
LOCUS       I57578                   15 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 115 from patent US 5610054.
ACCESSION   I57578
VERSION     I57578.1  GI:2482642
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Draper,K.G.
  TITLE     Enzymatic RNA molecule targeted against Hepatitis C virus
  JOURNAL   Patent: US 5610054-A 115 11-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 97;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTA 15
              | |||||||| ||
Db          2 GCCCCTACGTATA 14


RESULT 81
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AX048276
LOCUS       AX048276                 15 bp    RNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 12 from Patent WO0066780.
ACCESSION   AX048276
VERSION     AX048276.1  GI:11877041
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and
            Burger,C.
  TITLE     Adeno-associated virus-delivered ribozyme compositions and methods
            of use
  JOURNAL   Patent: WO 0066780-A 12 09-NOV-2000;
            University of Florida (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="SYNTHETIC PEPTIDE"

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 97;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCCAGG 28
              |||  ||||||||
Db          1 CAGACAGTCCAGG 13


RESULT 82
AX362585/c
LOCUS       AX362585                 15 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 19 from Patent WO0208425.
ACCESSION   AX362585
VERSION     AX362585.1  GI:18694729
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Finkel,K. and Koshy,B.
  TITLE     Haplotypes of the adrb3 gene
  JOURNAL   Patent: WO 0208425-A 19 31-JAN-2002;
            Genaissance Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 97;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAGT 23
              |||  ||||||||
Db         13 GTGCCCAGGGAGT 1


RESULT 83
BD207082
LOCUS       BD207082                 15 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection.
ACCESSION   BD207082
VERSION     BD207082.1  GI:33016852
KEYWORDS    JP 2002512791-A/672.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to hepatitis C virus infection
  JOURNAL   Patent: JP 2002512791-A 672 08-MAY-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Hepatitis virus (hepatitis C virus)
            PN   JP 2002512791-A/672
            PD   08-MAY-2002
            PF   26-APR-1999 JP 2000545991
            PR   27-APR-1998 US    60/083217,18-SEP-1998 US    60/100842 PR
            25-FEB-1999 US    09/257608,23-MAR-1999 US    09/274553 PI
            LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A  PI
            PAVCO,
            PI   DENNIS MACEJAK
            PC   C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
            PC   A61K37/66,
            PC   C12N15/00
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   hepatitis C virus infection.
            FH   Key             Location/Qualifiers
            FT   source          1. .15
            FT                   /organism='Hepatitis virus (hepatitis C  FT
                           virus)'.
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 97;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTA 15
              | ||||||| ||
Db          2 GCCCCTACGTATA 14


RESULT 84
AX625951/c
LOCUS       AX625951                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2992 from Patent WO02053774.
ACCESSION   AX625951
VERSION     AX625951.1  GI:28453989
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2992 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 64;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAG 22
              |||||||| ||
Db         11 TGTACAGGAAG 1


RESULT 85
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AX627912/c
LOCUS       AX627912                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4953 from Patent WO02053774.
ACCESSION   AX627912
VERSION     AX627912.1  GI:28455950
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4953 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 64;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAGG 28
              |||| ||||||
Db         11 GGGATTCCAGG 1


RESULT 86
AX628430/c
LOCUS       AX628430                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5471 from Patent WO02053774.
ACCESSION   AX628430
VERSION     AX628430.1  GI:28456468
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5471 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 64;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAGG 28
              |||||| ||||
Db         11 GGGAGTACAGG 1


RESULT 87
AX628528/c
LOCUS       AX628528                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5569 from Patent WO02053774.
ACCESSION   AX628528
VERSION     AX628528.1  GI:28456566
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5569 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 64;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAG 22
              ||||||||| |
Db         11 TGTACAGGGTG 1


RESULT 88
AR199211
LOCUS       AR199211                  12 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 67 from patent US 6355423.
ACCESSION   AR199211
VERSION     AR199211.1  GI:20249285
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Rothberg,J.Marc., Nallur,G.N. and Hu,X.
  TITLE     Methods and devices for measuring differential gene expression
  JOURNAL   Patent: US 6355423-A 67 12-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 76;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTAC 16
              ||||| |||||
Db          2 CCTACCTGTAC 12


RESULT 89
AR362486
LOCUS       AR362486                  12 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 2 from patent US 5174962.
ACCESSION   AR362486
VERSION     AR362486.1  GI:34422687
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Brennan,T.M.
  TITLE     Apparatus for determining DNA sequences by mass spectrometry
  JOURNAL   Patent: US 5174962-A 2 29-DEC-1992;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 76;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 ACGTGTACAGG 19
              ||||||||| |
Db          1 ACGTGTACACG 11
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RESULT 90
AR362486/c
LOCUS       AR362486                  12 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 2 from patent US 5174962.
ACCESSION   AR362486
VERSION     AR362486.1  GI:34422687
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Brennan,T.M.
  TITLE     Apparatus for determining DNA sequences by mass spectrometry
  JOURNAL   Patent: US 5174962-A 2 29-DEC-1992;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match           33.6%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 76;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 ACGTGTACAGG 19
              ||||||||| |
Db         12 ACGTGTACACG 2


RESULT 91
A42646/c
LOCUS       A42646                    14 bp    DNA     linear   PAT 06-MAR-1997
DEFINITION  Sequence 164 from Patent WO9502051.
ACCESSION   A42646
VERSION     A42646.1  GI:2298095
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Schlingensiepen,G., Schlingensiepen,R., Schlingensiepen,K. and
            Brysch,W.
  TITLE     A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR
            PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND
            CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS
  JOURNAL   Patent: WO 9502051-A 164 19-JAN-1995;
            BIOGNOSTIK GES FUER BIOMOLEKUL (DE)
COMMENT     Other publication AU 7345694 950206.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match           32.9%;  Score 9.2;  DB 1;  Length 14;
  Best Local Similarity   78.6%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACAGG 19
              |||  || ||||||
Db         14 CCTCTGTATACAGG 1


RESULT 92
A88835/c
LOCUS       A88835                    14 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 983 from Patent WO9833904.
ACCESSION   A88835
VERSION     A88835.1  GI:6737405
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 983 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match           32.9%;  Score 9.2;  DB 1;  Length 14;
  Best Local Similarity   78.6%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACAGG 19
              |||  || ||||||
Db         14 CCTCTGTATACAGG 1


RESULT 93
AR024070/c
LOCUS       AR024070                  14 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 20 from patent US 5795778.
ACCESSION   AR024070
VERSION     AR024070.1  GI:3977364
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Draper,K.G.
  TITLE     Method and reagent for inhibiting herpes simplex virus replication
  JOURNAL   Patent: US 5795778-A 20 18-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match           32.9%;  Score 9.2;  DB 1;  Length 14;
  Best Local Similarity   78.6%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGT 23
              ||||  ||||| ||
Db         14 CGTGATCAGGGCGT 1


RESULT 94
AR224289/c
LOCUS       AR224289                  14 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 20 from patent US 6440719.
ACCESSION   AR224289
VERSION     AR224289.1  GI:23333066
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Draper,K.G.
  TITLE     Method and reagent for inhibiting herpes simplex virus replication
  JOURNAL   Patent: US 6440719-A 20 27-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match           32.9%;  Score 9.2;  DB 1;  Length 14;
  Best Local Similarity   78.6%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGT 23
```

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                ||||  |||||  ||
Db          14 CGTGATCAGGGCGT 1


RESULT 95
AX711052/c
LOCUS       AX711052                  14 bp    RNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 352 from Patent EP1288296.
ACCESSION   AX711052
VERSION     AX711052.1  GI:29787433
KEYWORDS    .
SOURCE      Herpes simplex virus unknown type
  ORGANISM  Herpes simplex virus unknown type
            Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
            Alphaherpesvirinae; Simplexvirus.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 352 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Herpes simplex virus unknown type"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:126283"

  Query Match             32.9%;  Score 9.2;  DB 1;  Length 14;
  Best Local Similarity   78.6%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          10 CGTGTACAGGGAGT 23
                ||||  |||||  ||
Db          14 CGTGATCAGGGCGT 1


RESULT 96
BD001174/c
LOCUS       BD001174                  14 bp    RNA     linear   PAT 31-JAN-2002
DEFINITION  Method and reagent for inhibiting viral replication.
ACCESSION   BD001174
VERSION     BD001174.1  GI:18625733
KEYWORDS    JP 2000342285-A/334.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
            Holesek,J.J. and Mamone,A.J.
  TITLE     Method and reagent for inhibiting viral replication
  JOURNAL   Patent: JP 2000342285-A 334 12-DEC-2000;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000342285-A/334
            PD   12-DEC-2000
            PF   01-MAY-2000 JP 2000132616
            PR   11-MAY-1992 US    07/882689,14-MAY-1992 US    07/882712 PR
            14-MAY-1992 US    07/882713,14-MAY-1992 US    07/882714 PR
            14-MAY-1992 US    07/882823,14-MAY-1992 US    07/882824 PR
            14-MAY-1992 US    07/882886,14-MAY-1992 US    07/882888 PR
            14-MAY-1992 US    07/882889,14-MAY-1992 US    07/882921 PR
            14-MAY-1992 US    07/882922,14-MAY-1992 US    07/883823 PR
            14-MAY-1992 US    07/883849,14-MAY-1992 US    07/884073 PR
            14-MAY-1992 US    07/884074,14-MAY-1992 US    07/884333 PR
            14-MAY-1992 US    07/884422,14-MAY-1992 US    07/884431 PR
            14-MAY-1992 US    07/884436,14-MAY-1992 US    07/884521 PR
            31-JUL-1992 US    07/923738,26-AUG-1992 US    07/935854 PR
            26-AUG-1992 US    07/936086,18-SEP-1992 US    07/948359 PR
            15-OCT-1992 US    07/963322,07-DEC-1992 US    07/987129 PR
            07-DEC-1992 US    07/987130,07-DEC-1992 US    07/987133 PI
            KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN, PI   DENNIS G
            MAYSEJAK,
            PI   JAMES J HOLESEK,ANTHONY J MAMONE
            PC   C12N15/09,C12N5/10,C12N7/00,C12N9/22//(C12N5/10,C12R1:91), PC
             C12N15/00,
            PC   C12N5/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"

  Query Match             32.9%;  Score 9.2;  DB 1;  Length 14;
  Best Local Similarity   78.6%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          10 CGTGTACAGGGAGT 23
                ||||  |||||  ||
Db          14 CGTGATCAGGGCGT 1


RESULT 97
BD001603/c
LOCUS       BD001603                  14 bp    RNA     linear   PAT 31-JAN-2002
DEFINITION  Method and reagent for inhibiting viral replication.
ACCESSION   BD001603
VERSION     BD001603.1  GI:18626162
KEYWORDS    JP 2000342286-A/334.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
            Holesek,J.J. and Mamone,A.J.
  TITLE     Method and reagent for inhibiting viral replication
  JOURNAL   Patent: JP 2000342286-A 334 12-DEC-2000;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000342286-A/334
            PD   12-DEC-2000
            PF   01-MAY-2000 JP 2000132651
            PR   11-MAY-1992 US    07/882689,14-MAY-1992 US    07/882712 PR
            14-MAY-1992 US    07/882713,14-MAY-1992 US    07/882714 PR
            14-MAY-1992 US    07/882823,14-MAY-1992 US    07/882824 PR
            14-MAY-1992 US    07/882886,14-MAY-1992 US    07/882888 PR
            14-MAY-1992 US    07/882889,14-MAY-1992 US    07/882921 PR
            14-MAY-1992 US    07/882922,14-MAY-1992 US    07/883823 PR
            14-MAY-1992 US    07/883849,14-MAY-1992 US    07/884073 PR
            14-MAY-1992 US    07/884074,14-MAY-1992 US    07/884333 PR
            14-MAY-1992 US    07/884422,14-MAY-1992 US    07/884431 PR
            14-MAY-1992 US    07/884436,14-MAY-1992 US    07/884521 PR
            31-JUL-1992 US    07/923738,26-AUG-1992 US    07/935854 PR
            26-AUG-1992 US    07/936086,18-SEP-1992 US    07/948359 PR
            15-OCT-1992 US    07/963322,07-DEC-1992 US    07/987129 PR
            07-DEC-1992 US    07/987130,07-DEC-1992 US    07/987133 PI
            KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN, PI   DENNIS G
            MAYSEJAK,
            PI   JAMES J HOLESEK,ANTHONY J MAMONE
            PC   C12N15/09,C12N5/10,C12N7/00//A61K38/43,A61K39/125,A61K39/13,
            PC   A61K39/135,
            PC   A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
            PC   A61P1/16,
            PC   A61P31/14,A61P31/16,A61P31/18,A61P31/22,A61P35/02,C12Q1/68, PC
              (C12N15/09,C12R1:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00, PC
             C12R1:93)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="synthetic construct"
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                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"

  Query Match             32.9%;  Score 9.2;  DB 1;  Length 14;
  Best Local Similarity   78.6%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGT 23
              ||||  |||||  ||
Db         14 CGTGATCAGGGCGT 1


RESULT 98
BD066348/c
LOCUS       BD066348                 14 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  An antisense oligonucleotide preparation method.
ACCESSION   BD066348
VERSION     BD066348.1  GI:22611951
KEYWORDS    JP 2001511000-A/983.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Schlingensiepen,K.H. and Brysch,W.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: JP 2001511000-A 983 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS   Unknown
            PN   JP 2001511000-A/983
            PD   07-AUG-2001
            PF   30-JAN-1998 JP 1998532533
            PR   31-JAN-1997 EP   97101531.8
            PI   KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC   C12N15/11,C07H21/04,A61K31/70
            CC   An antisense oligonucleotide preparation method FH   Key
                 Location/Qualifiers
            FT   source          1. .14
            FT                   /organism='Unknown'.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             32.9%;  Score 9.2;  DB 1;  Length 14;
  Best Local Similarity   78.6%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACAGG 19
              |||  || ||||||
Db         14 CCTCTGTATACAGG 1


RESULT 99
AX152114
LOCUS       AX152114                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 29 from Patent WO0138577.
ACCESSION   AX152114
VERSION     AX152114.1  GI:14533765
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 29 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             32.1%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GAGTCCAGG 28
              |||||||||
Db          2 GAGTCCAGG 10


RESULT 100
AX626581/c
LOCUS       AX626581                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3622 from Patent WO02053774.
ACCESSION   AX626581
VERSION     AX626581.1  GI:28454619
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3622 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             32.1%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 79;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCAG 27
              |||||||||
Db          9 GGAGTCCAG 1


RESULT 101
AX628461/c
LOCUS       AX628461                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5502 from Patent WO02053774.
ACCESSION   AX628461
VERSION     AX628461.1  GI:28456499
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5502 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             32.1%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 79;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              |||||||||
Db         11 TACGTGTAC 3
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RESULT 102
A47646/c
LOCUS       A47646                    12 bp    DNA     linear   PAT 07-MAR-1997
DEFINITION  Sequence 6 from Patent EP0692535.
ACCESSION   A47646
VERSION     A47646.1  GI:2301587
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Colote,S. and Pirotzky,E.
  TITLE     Oligonucleotides to inhibit the role of isoprenyl protein
            transferases
  JOURNAL   Patent: EP 0692535-A 6 17-JAN-1996;
            SOD CONSEILS RECH APPLIC (FR)
COMMENT     Other publication CN 1124142 960612
            Other publication CZ 9501688 960515
            Other publication BR 9503015 960604
            Other publication NZ 272398 960426
            Other publication HU 72133 960328
            Other publication JP 8051985 960227
            Other publication FR 2721930 960105
            Other publication FR 2721827 960105
            Other publication FI 953170 951230
            Other publication SE 9502259 951230
            Other publication PL 309384 960108
            Other publication NO 952601 960102
            Other publication AU 2329995 960111
            Other publication CA 2152233 951230
            Other publication GB 2290791 960110.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             32.1%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 94;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 GTACAGGGA 21
               |||||||||
Db          12 GTACAGGGA 4


RESULT 103
AR027864/c
LOCUS       AR027864                  12 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 6 from patent US 5856461.
ACCESSION   AR027864
VERSION     AR027864.1  GI:5938684
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Colote,S. and Pirotzky,E.
  TITLE     Oligonucleotides to inhibit the expression of isoprenyl protein
            transferases
  JOURNAL   Patent: US 5856461-A 6 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             32.1%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 94;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 GTACAGGGA 21
               |||||||||
Db          12 GTACAGGGA 4


RESULT 104
BD259424/c
LOCUS       BD259424                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD259424
VERSION     BD259424.1  GI:33069194
KEYWORDS    JP 2002541795-A/7217.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 7217 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/7217
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             32.1%;  Score 9;  DB 1;  Length 17;
  Best Local Similarity   70.6%;  Pred. No. 1.8e+02;
  Matches   12;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy           6 CCTACGTGTACAGGGAG 22
               ||| |  ||||| | ||
Db          17 CCTCCTGGTACATGTAG 1


RESULT 105
AR199211/c
LOCUS       AR199211                  12 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 67 from patent US 6355423.
ACCESSION   AR199211
VERSION     AR199211.1  GI:20249285
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Rothberg,J.Marc., Nallur,G.N. and Hu,X.
  TITLE     Methods and devices for measuring differential gene expression
  JOURNAL   Patent: US 6355423-A 67 12-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 1e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy          13 GTACAGGGAGTC 24
               ||||||| || |
Db          12 GTACAGGTAGGC 1


RESULT 106
A97287
LOCUS       A97287                    12 bp    DNA     linear   PAT 26-JAN-2000
DEFINITION  Sequence 4 from Patent WO9918197.
ACCESSION   A97287
VERSION     A97287.1  GI:6780670
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Yaspo,M. and Lehrach,H.
  TITLE     NUCLEIC ACID MOLECULE ENCODING A (POLY)PEPTIDE CO-SEGREGATING IN
            MUTATED FORM WITH AUTOIMMUNE POLYENDOCRINOPATHY CANDIDIASIS
            ECTODERMAL DYSTROPHY (APECED)
  JOURNAL   Patent: WO 9918197-A 4 15-APR-1999;
            MAX PLANCK GESELLSCHAFT (DE); YASPO MARIE LAURE (DE)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 1e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          15 ACAGGGAGTCCA 26
               ||||| || |||
Db           1 ACAGGCAGGCCA 12


RESULT 107
AR167847/c
LOCUS       AR167847                  12 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 211 from patent US 6287769.
ACCESSION   AR167847
VERSION     AR167847.1  GI:17903654
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Inoue,T.
  TITLE     Method of amplifying DNA fragment, apparatus for amplifying DNA
            fragment, method of assaying microorganisms, method of analyzing
            microorganisms and method of assaying contaminant
  JOURNAL   Patent: US 6287769-A 211 11-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 1e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           5 CCCTACGTGTAC 16
               || |||||| ||
Db          12 CCATACGTGCAC 1


RESULT 108
E29731/c
LOCUS       E29731                    12 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for amplifying DNA fragment, method for estimating state of
            microorganism existing and method for estimating state of waste.
ACCESSION   E29731
VERSION     E29731.1  GI:13021234
KEYWORDS    JP 1999276176-A/211.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Koichi,I.
  TITLE     Method for amplifying DNA fragment, method for estimating state of
            microorganism existing and method for estimating state of waste
  JOURNAL   Patent: JP 1999276176-A 211 12-OCT-1999;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
COMMENT     OS   Unidentified
            PN   JP 1999276176-A/211
            PD   12-OCT-1999
            PF   31-MAR-1998 JP 1998087652
            PR
            PI   KOICHI INOUE
            PC   C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC
            Strandedness: Single;
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 1e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           5 CCCTACGTGTAC 16
               || |||||| ||
Db          12 CCATACGTGCAC 1


RESULT 109
E38837/c
LOCUS       E38837                    12 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method and device for amplifying DNA fragment.
ACCESSION   E38837
VERSION     E38837.1  GI:18621499
KEYWORDS    JP 2000270867-A/211.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Inoue,K.
  TITLE     Method and device for amplifying DNA fragment
  JOURNAL   Patent: JP 2000270867-A 211 03-OCT-2000;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
COMMENT     OS   Unidentified
            PN   JP 2000270867-A/211
            PD   03-OCT-2000
            PF   19-MAR-1999 JP 1999076844
            PR
            PI   KOICHI INOUE
            PC   C12N15/09,C12M1/00,C12Q1/68,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
```

```
  Best Local Similarity   83.3%;  Pred. No. 1e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTAC 16
              || |||||| ||
Db         12 CCATACGTGCAC 1


RESULT 110
E64263/c
LOCUS       E64263                    12 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for amplifying DNA fragment, amplification apparatus of DNA
            fragment, method for assaying a group of microorganisms, method
            for analyzing a group of microorganisms, and method for assaying
            contaminating  substance.
ACCESSION   E64263
VERSION     E64263.1  GI:13019667
KEYWORDS    JP 1999341989-A/211.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Koichi,I.
  TITLE     Method for amplifying DNA fragment, amplification apparatus of DNA
            fragment, method for assaying a group of microorganisms, method for
            analyzing a group of microorganisms, and method for assaying
            contaminating substance
  JOURNAL   Patent: JP 1999341989-A 211 14-DEC-1999;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
COMMENT     OS   Artificial Sequence
            PN   JP 1999341989-A/211
            PD   14-DEC-1999
            PF   16-MAR-1999 JP 1999069694
            PR
            PI   KOICHI INOUE
            PC   C12N15/09,C12M1/00,C12Q1/68,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 1e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTAC 16
              || |||||| ||
Db         12 CCATACGTGCAC 1


RESULT 111
AR407937
LOCUS       AR407937                  13 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 30 from patent US 6632057.
ACCESSION   AR407937
VERSION     AR407937.1  GI:40157924
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Fauchet,C.R.J.
  TITLE     Fixing unit with an end imprint in a threaded terminal portion
  JOURNAL   Patent: US 6632057-A 30 14-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 1.2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCTACGT 12
              | ||| ||||||
Db          1 CAGGCTCTACGT 12


RESULT 112
AR088591/c
LOCUS       AR088591                  10 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 7 from patent US 5989906.
ACCESSION   AR088591
VERSION     AR088591.1  GI:10015355
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Thompson,J.D.
  TITLE     Method and reagent for inhibiting P-glycoprotein (mdr-1-gene)
  JOURNAL   Patent: US 5989906-A 7 23-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 89;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              || |||||||
Db         10 GGAAGTCCAG 1


RESULT 113
AR099558/c
LOCUS       AR099558                  10 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 85 from patent US 6077833.
ACCESSION   AR099558
VERSION     AR099558.1  GI:12809324
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Bennett,C.Frank. and Vickers,T.A.
  TITLE     Oligonucleotide compositions and methods for the modulation of the
            expression of B7 protein
  JOURNAL   Patent: US 6077833-A 85 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 89;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAG 22
              |||| |||||
Db         10 GTACGGGGAG 1


RESULT 114
AR178839/c
LOCUS       AR178839                  10 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 85 from patent US 6319906.
ACCESSION   AR178839
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VERSION     AR178839.1  GI:20219977
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Bennett,C.Frank. and Vickers,T.A.
  TITLE     Oligonucleotide compositions and methods for the modulation of the
            expression of B7 protein
  JOURNAL   Patent: US 6319906-A 85 20-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 89;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          13 GTACAGGGAG 22
               |||| |||||
Db          10 GTACGGGGAG 1


RESULT 115
E54652/c
LOCUS       E54652                    10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human normal liver cell expression genes.
ACCESSION   E54652
VERSION     E54652.1  GI:22556135
KEYWORDS    JP 2001211883-A/4.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human normal liver cell expression genes
  JOURNAL   Patent: JP 2001211883-A 4 07-AUG-2001;
            SCIENCE & TECH AGENCY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001211883-A/4
            PD   07-AUG-2001
            PF   31-JAN-2000 JP 2000023170
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K16/18,C12P21/02,C12N15/00
            CC
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 89;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          18 GGGAGTCCAG 27
               ||||| ||||
Db          10 GGGAGGCCAG 1


RESULT 116
AR336839
LOCUS       AR336839                  10 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 14 from patent US 6566130.
ACCESSION   AR336839
VERSION     AR336839.1  GI:33722689
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
  TITLE     Androgen-regulated gene expressed in prostate tissue
  JOURNAL   Patent: US 6566130-A 14 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 89;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          13 GTACAGGGAG 22
               || |||||||
Db          1 GTGCAGGGAG 10


RESULT 117
AX113024/c
LOCUS       AX113024                  10 bp    DNA     linear   PAT 01-MAY-2001
DEFINITION  Sequence 71 from Patent WO0127267.
ACCESSION   AX113024
VERSION     AX113024.1  GI:13939459
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Adams,E., Waldmann,H., Cobbold,S. and Zelenika,D.
  TITLE     Genes differentially expressed in tr1 cells and their use in the
            manufacture of immunoregulatory compositions
  JOURNAL   Patent: WO 0127267-A 71 19-APR-2001;
            ISIS INNOVATION LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Mus sp."
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10095"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 89;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGA 21
               ||||| ||||
Db          10 TGTACGGGGA 1


RESULT 118
AX153342/c
LOCUS       AX153342                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1257 from Patent WO0138577.
ACCESSION   AX153342
VERSION     AX153342.1  GI:14534993
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1257 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 89;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGA 21
               ||||| ||||
Db          10 TGTACGGGGA 1


RESULT 119
AX377356
LOCUS       AX377356                 10 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 20 from Patent WO0212499.
ACCESSION   AX377356
VERSION     AX377356.1  GI:19573642
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kliem,S.E., Koshy,B. and Lanz,E.M.
  TITLE     Haplotypes of the ntf3 gene
  JOURNAL   Patent: WO 0212499-A 20 14-FEB-2002;
            Genaissance Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 89;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCTAC 10
              |||||||| |
Db          1 CGGGCCCTCC 10


RESULT 120
BD166783/c
LOCUS       BD166783                 10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD166783
VERSION     BD166783.1  GI:27872595
KEYWORDS    JP 2002209591-A/328.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 328 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/328
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 89;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          17 AGGGAGTCCA 26
               |||| |||||
Db          10 AGGGCGTCCA 1


RESULT 121
BD167020/c
LOCUS       BD167020                 10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD167020
VERSION     BD167020.1  GI:27872832
KEYWORDS    JP 2002209591-A/565.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 565 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/565
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 89;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          17 AGGGAGTCCA 26
               |||| |||||
Db          10 AGGGCGTCCA 1


RESULT 122
BD167059/c
LOCUS       BD167059                 10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD167059
VERSION     BD167059.1  GI:27872871
KEYWORDS    JP 2002209591-A/604.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 604 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/604
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
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            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 89;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          18 GGGAGTCCAG 27
               ||||| ||||
Db          10 GGGAGGCCAG 1


RESULT 123
BD167158/c
LOCUS       BD167158                 10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD167158
VERSION     BD167158.1  GI:27872970
KEYWORDS    JP 2002209591-A/703.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 703 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/703
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 89;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          18 GGGAGTCCAG 27
               ||||| ||||
Db          10 GGGAGGCCAG 1


RESULT 124
AR099559/c
LOCUS       AR099559                 11 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 86 from patent US 6077833.
ACCESSION   AR099559
VERSION     AR099559.1  GI:12809325
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Bennett,C.Frank. and Vickers,T.A.
  TITLE     Oligonucleotide compositions and methods for the modulation of the
            expression of B7 protein
  JOURNAL   Patent: US 6077833-A 86 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          13 GTACAGGGAG 22
               |||| |||||
Db          11 GTACGGGGAG 2


RESULT 125
AR178840/c
LOCUS       AR178840                 11 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 86 from patent US 6319906.
ACCESSION   AR178840
VERSION     AR178840.1  GI:20219978
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Bennett,C.Frank. and Vickers,T.A.
  TITLE     Oligonucleotide compositions and methods for the modulation of the
            expression of B7 protein
  JOURNAL   Patent: US 6319906-A 86 20-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          13 GTACAGGGAG 22
               |||| |||||
Db          11 GTACGGGGAG 2


RESULT 126
BD241058
LOCUS       BD241058                 11 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Methods and products related to genotyping and DNA analysis.
ACCESSION   BD241058
VERSION     BD241058.1  GI:33050828
KEYWORDS    JP 2002525127-A/5.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Landers,J.E., Jordan,B., Housman,D.E. and Charest,A.
  TITLE     Methods and products related to genotyping and DNA analysis
  JOURNAL   Patent: JP 2002525127-A 5 13-AUG-2002;
            MASSACHUSETTS INSTITUTE OF TECHNOLOGY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002525127-A/5
            PD   13-AUG-2002
            PF   24-SEP-1999 JP 2000572407
            PR   25-SEP-1998 US    60/101757
            PI   JOHN E LANDERS,BARBARA JORDAN,DAVID E HOUSMAN,ALAIN CHAREST PC
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            C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N33/58,G01N37/00, PC
           G01N37/00,
           PC   C12N15/00
           CC   Methods and products related to genotyping and DNA analysis FH
             Key             Location/Qualifiers
           FT   source          1. .11
           FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACA 17
              || |||||||
Db          1 TAAGTGTACA 10


RESULT 127
AR301464/c
LOCUS       AR301464                  11 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 45 from patent US 6538173.
ACCESSION   AR301464
VERSION     AR301464.1  GI:31689266
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Heber-Katz,E.
  TITLE     Compositions and methods for wound healing
  JOURNAL   Patent: US 6538173-A 45 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGA 21
              ||||| ||||
Db         10 TGTACGGGGA 1


RESULT 128
AX099043
LOCUS       AX099043                  11 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 106 from Patent WO0120026.
ACCESSION   AX099043
VERSION     AX099043.1  GI:13538253
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wojnowski,L. and Hustert,E.
  TITLE     Polymorphisms in the human hpxr gene and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 0120026-A 106 22-MAR-2001;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="artificial sequence"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              |||||| |||
Db          2 GGGAGTGCAG 11


RESULT 129
AX099044/c
LOCUS       AX099044                  11 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 107 from Patent WO0120026.
ACCESSION   AX099044
VERSION     AX099044.1  GI:13538254
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wojnowski,L. and Hustert,E.
  TITLE     Polymorphisms in the human hpxr gene and their use in diagnostic
            and therapeutic applications
  JOURNAL   Patent: WO 0120026-A 107 22-MAR-2001;
            Epidauros Biotechnologie AG (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="artificial sequence"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              |||||| |||
Db         10 GGGAGTGCAG 1


RESULT 130
AX470626/c
LOCUS       AX470626                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 203 from Patent WO02053773.
ACCESSION   AX470626
VERSION     AX470626.1  GI:22205751
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 203 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAG 22
              || |||||||
Db         10 GTTCAGGGAG 1


RESULT 131
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AX470645
LOCUS       AX470645                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 222 from Patent WO02053773.
ACCESSION   AX470645
VERSION     AX470645.1  GI:22205770
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 222 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCTAC 10
              | ||||||||
Db          1 CCGGCCCTAC 10


RESULT 132
AX470757
LOCUS       AX470757                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 334 from Patent WO02053773.
ACCESSION   AX470757
VERSION     AX470757.1  GI:22205882
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 334 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              |||| |||||
Db          2 GGGACTCCAG 11


RESULT 133
AX470853
LOCUS       AX470853                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 430 from Patent WO02053773.
ACCESSION   AX470853
VERSION     AX470853.1  GI:22205978
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 430 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCAGG 28
              |||| |||||
Db          2 GGAGGCCAGG 11


RESULT 134
AX471193/c
LOCUS       AX471193                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 770 from Patent WO02053773.
ACCESSION   AX471193
VERSION     AX471193.1  GI:22206318
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 770 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCC 25
              ||| ||||||
Db         11 CAGTGAGTCC 2


RESULT 135
AX472098
LOCUS       AX472098                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 89 from Patent WO02053775.
ACCESSION   AX472098
VERSION     AX472098.1  GI:22207139
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hustert,E., Haberl,M. and Wojnowski,L.
  TITLE     Identification of the genetic determinants of the polymorphic
            cyp3a5 expression
  JOURNAL   Patent: WO 02053775-A 89 11-JUL-2002;
            EPIDAUROS BIOTECHNOLOGIE AG (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAG 22
              ||||||| ||
Db          1 GTACAGGAAG 10


RESULT 136
AX623332
LOCUS       AX623332                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 373 from Patent WO02053774.
ACCESSION   AX623332
VERSION     AX623332.1  GI:28451273
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 373 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTG 13
              ||||||| ||
Db          1 GCCCTACCTG 10


RESULT 137
AX623370/c
LOCUS       AX623370                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 411 from Patent WO02053774.
ACCESSION   AX623370
VERSION     AX623370.1  GI:28451311
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 411 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              ||||||| ||
Db         11 GGGAGTCAAG 2


RESULT 138
AX623664/c
LOCUS       AX623664                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 705 from Patent WO02053774.
ACCESSION   AX623664
VERSION     AX623664.1  GI:28451605
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 705 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGG 20
              | ||||||||
Db         11 GAGTACAGGG 2


RESULT 139
AX623917
LOCUS       AX623917                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 958 from Patent WO02053774.
ACCESSION   AX623917
VERSION     AX623917.1  GI:28451858
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 958 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCAGG 28
              ||| ||||||
Db          2 GGAATCCAGG 11


RESULT 140
AX624031/c
LOCUS       AX624031                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 1072 from Patent WO02053774.
ACCESSION   AX624031
VERSION     AX624031.1  GI:28451972
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
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  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 1072 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAG 22
              || |||||||
Db         10 GTTCAGGGAG 1


RESULT 141
AX624952
LOCUS       AX624952                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 1993 from Patent WO02053774.
ACCESSION   AX624952
VERSION     AX624952.1  GI:28452893
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 1993 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCTAC 10
              | ||||||||
Db          1 CCGGCCCTAC 10


RESULT 142
AX625222/c
LOCUS       AX625222                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2263 from Patent WO02053774.
ACCESSION   AX625222
VERSION     AX625222.1  GI:28453163
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2263 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 ACGTGTACAG 18
              | ||||||||
Db         11 AGGTGTACAG 2


RESULT 143
AX625736
LOCUS       AX625736                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2777 from Patent WO02053774.
ACCESSION   AX625736
VERSION     AX625736.1  GI:28453677
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2777 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              |||| |||||
Db          2 GGGACTCCAG 11


RESULT 144
AX627101
LOCUS       AX627101                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4142 from Patent WO02053774.
ACCESSION   AX627101
VERSION     AX627101.1  GI:28455139
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4142 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGG 20
              |||| |||||
Db          2 GTGTTCAGGG 11


RESULT 145
AX629184
LOCUS       AX629184                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6225 from Patent WO02053774.
```

```
ACCESSION   AX629184
VERSION     AX629184.1  GI:28457222
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6225 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCAGG 28
              |||| |||||
Db          2 GGAGGCCAGG 11


RESULT 146
AX629283/c
LOCUS       AX629283                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6324 from Patent WO02053774.
ACCESSION   AX629283
VERSION     AX629283.1  GI:28457321
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6324 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAGTC 24
              |||| |||||
Db         10 ACAGAGAGTC 1


RESULT 147
AX629976/c
LOCUS       AX629976                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7017 from Patent WO02053774.
ACCESSION   AX629976
VERSION     AX629976.1  GI:28458014
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7017 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCC 25
              ||| ||||||
Db         11 CAGTGAGTCC 2


RESULT 148
AX630753
LOCUS       AX630753                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7794 from Patent WO02053774.
ACCESSION   AX630753
VERSION     AX630753.1  GI:28458791
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7794 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTG 13
              ||||||| ||
Db          1 GCCCTACCTG 10


RESULT 149
AX630791/c
LOCUS       AX630791                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7832 from Patent WO02053774.
ACCESSION   AX630791
VERSION     AX630791.1  GI:28458831
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7832 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          18 GGGAGTCCAG 27
               ||||||| ||
Db          11 GGGAGTCAAG 2


RESULT 150
AX631085/c
LOCUS       AX631085                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 8126 from Patent WO02053774.
ACCESSION   AX631085
VERSION     AX631085.1  GI:28459129
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8126 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          11 GTGTACAGGG 20
               | ||||||||
Db          11 GAGTACAGGG 2


RESULT 151
AX631338
LOCUS       AX631338                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 8380 from Patent WO02053774.
ACCESSION   AX631338
VERSION     AX631338.1  GI:28459384
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8380 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          19 GGAGTCCAGG 28
               ||| ||||||
Db           2 GGAATCCAGG 11


RESULT 152
AX631452/c
LOCUS       AX631452                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 8494 from Patent WO02053774.
ACCESSION   AX631452
VERSION     AX631452.1  GI:28459518
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8494 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          13 GTACAGGGAG 22
               || |||||||
Db          10 GTTCAGGGAG 1


RESULT 153
AX632373
LOCUS       AX632373                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9415 from Patent WO02053774.
ACCESSION   AX632373
VERSION     AX632373.1  GI:28467988
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9415 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           1 CGGGCCCTAC 10
               | ||||||||
Db           1 CCGGCCCTAC 10


RESULT 154
AX632643/c
LOCUS       AX632643                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9685 from Patent WO02053774.
ACCESSION   AX632643
VERSION     AX632643.1  GI:28468258
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9685 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
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     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 ACGTGTACAG 18
              | ||||||||
Db         11 AGGTGTACAG 2


RESULT 155
BD124214/c
LOCUS       BD124214                  11 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Compositions and method for healing wound.
ACCESSION   BD124214
VERSION     BD124214.1  GI:23219159
KEYWORDS    JP 2002503460-A/45.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Katz,E.H.
  TITLE     Compositions and method for healing wound
  JOURNAL   Patent: JP 2002503460-A 45 05-FEB-2002;
            THE WISTAR INSTITUTE
COMMENT     OS   Mus musculus (mouse)
            PN   JP 2002503460-A/45
            PD   05-FEB-2002
            PF   12-FEB-1999 JP 2000531545
            PR   13-FEB-1998 US    60/074737,26-AUG-1998 US    60/097937 PR
            28-SEP-1998 US    60/102051
            PI   ELLEN HEBER KATZ
            PC   C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
              C12N5/00
            CC   Compositions and method for healing wound
            FH   Key             Location/Qualifiers
            FT   source          1. .11
            FT                   /organism='Mus musculus (mouse)'.
FEATURES            Location/Qualifiers
     source         1. .11
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:10090"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGA 21
              ||||| ||||
Db         10 TGTACGGGGA 1


RESULT 156
A47668/c
LOCUS       A47668                    12 bp    DNA     linear   PAT 07-MAR-1997
DEFINITION  Sequence 28 from Patent EP0692535.
ACCESSION   A47668
VERSION     A47668.1  GI:2301609
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Colote,S. and Pirotzky,E.
  TITLE     Oligonucleotides to inhibit the role of isoprenyl protein
            transferases
  JOURNAL   Patent: EP 0692535-A 28 17-JAN-1996;
            SOD CONSEILS RECH APPLIC (FR)
COMMENT     Other publication CN 1124142 960612
            Other publication CZ 9501688 960515
            Other publication BR 9503015 960604
            Other publication NZ 272398 960426
            Other publication HU 72133 960328
            Other publication JP 8051985 960227
            Other publication FR 2721930 960105
            Other publication FR 2721827 960105
            Other publication FI 953170 951230
            Other publication SE 9502259 951230
            Other publication PL 309384 960108
            Other publication NO 952601 960102
            Other publication AU 2329995 960111
            Other publication CA 2152233 951230
            Other publication GB 2290791 960110.
FEATURES            Location/Qualifiers
     source         1. .12
                    /organism="unidentified"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32644"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 ACGTGTACAG 18
              ||| ||||||
Db         11 ACGAGTACAG 2


RESULT 157
AR024089
LOCUS       AR024089                  12 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 39 from patent US 5795778.
ACCESSION   AR024089
VERSION     AR024089.1  GI:3977383
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Draper,K.G.
  TITLE     Method and reagent for inhibiting herpes simplex virus replication
  JOURNAL   Patent: US 5795778-A 39 18-AUG-1998;
FEATURES            Location/Qualifiers
     source         1. .12
                    /organism="unknown"
                    /mol_type="unassigned DNA"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGT 14
              ||| ||||||
Db          1 CCCGACGTGT 10


RESULT 158
AR027886/c
LOCUS       AR027886                  12 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 28 from patent US 5856461.
ACCESSION   AR027886
VERSION     AR027886.1  GI:5938706
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Colote,S. and Pirotzky,E.
  TITLE     Oligonucleotides to inhibit the expression of isoprenyl protein
            transferases
```

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  JOURNAL   Patent: US 5856461-A 28 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 ACGTGTACAG 18
              ||| ||||||
Db         11 ACGAGTACAG 2


RESULT 159
AR099560/c
LOCUS       AR099560                  12 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 87 from patent US 6077833.
ACCESSION   AR099560
VERSION     AR099560.1  GI:12809326
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Bennett,C.Frank. and Vickers,T.A.
  TITLE     Oligonucleotide compositions and methods for the modulation of the
            expression of B7 protein
  JOURNAL   Patent: US 6077833-A 87 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          13 GTACAGGGAG 22
               |||| |||||
Db          12 GTACGGGGAG 3


RESULT 160
AR167743/c
LOCUS       AR167743                  12 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 107 from patent US 6287769.
ACCESSION   AR167743
VERSION     AR167743.1  GI:17903543
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Inoue,T.
  TITLE     Method of amplifying DNA fragment, apparatus for amplifying DNA
            fragment, method of assaying microorganisms, method of analyzing
            microorganisms and method of assaying contaminant
  JOURNAL   Patent: US 6287769-A 107 11-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           7 CTACGTGTAC 16
               || |||||||
Db          12 CTTCGTGTAC 3


RESULT 161
AR178738
LOCUS       AR178738                  12 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 25 from patent US 6319714.
ACCESSION   AR178738
VERSION     AR178738.1  GI:20219876
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Crameri,A., Stemmer,W.P.C., Minshull,J., Bass,S.H., Welch,M.,
            Ness,J.E., Gustafsson,C. and Patten,P.A.
  TITLE     Oligonucleotide mediated nucleic acid recombination
  JOURNAL   Patent: US 6319714-A 25 20-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          18 GGGAGTCCAG 27
               ||| ||||||
Db           2 GGGGGTCCAG 11


RESULT 162
AR178841/c
LOCUS       AR178841                  12 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 87 from patent US 6319906.
ACCESSION   AR178841
VERSION     AR178841.1  GI:20219979
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Bennett,C.Frank. and Vickers,T.A.
  TITLE     Oligonucleotide compositions and methods for the modulation of the
            expression of B7 protein
  JOURNAL   Patent: US 6319906-A 87 20-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          13 GTACAGGGAG 22
               |||| |||||
Db          12 GTACGGGGAG 3


RESULT 163
BD251252
LOCUS       BD251252                  12 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotide mediated nucleic acid recombination.
ACCESSION   BD251252
VERSION     BD251252.1  GI:33061022
KEYWORDS    JP 2002534966-A/25.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Crameri,A., Stemmer,W.P.C., Minshull,J., Bass,S.H., Welch,M.,
            Ness,J.E., Gustafsson,C. and Patten,P.A.
```

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  TITLE     Oligonucleotide mediated nucleic acid recombination
  JOURNAL   Patent: JP 2002534966-A 25 22-OCT-2002;
            MAXYGEN INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534966-A/25
            PD   22-OCT-2002
            PF   18-JAN-2000 JP 2000594068
            PR   19-JAN-1999 US    60/116447,05-FEB-1999 US    60/118813 PR
            05-FEB-1999 US    60/118854,24-JUN-1999 US    60/141049 PR
            28-SEP-1999 US    09/408392,28-SEP-1999 US    09/408393 PR
            12-OCT-1999 US    09/416375,12-OCT-1999 US    09/416837 PI
            ANDREAS CRAMERI,WILLEM P C STEMMER,JEREMY MINSHULL,STEVEN H  PI
            BASS,
            PI   MARK WELCH,JON E NESS,CLAES GUSTAFSSON,PHILLIP A PATTEN PC
            C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N7/00,C12Q1/ PC
            68,C12N15/00,
            PC   C12N5/00
            CC   Oligonucleotide mediated nucleic acid recombination FH   Key
                      Location/Qualifiers
            FT   CDS              (1). .(12).
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match            30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          18 GGGAGTCCAG 27
               ||| ||||||
Db           2 GGGGGTCCAG 11


RESULT 164
E29627/c
LOCUS       E29627                    12 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for amplifying DNA fragment, method for estimating state of
            microorganism existing and method for estimating state of waste.
ACCESSION   E29627
VERSION     E29627.1  GI:13021130
KEYWORDS    JP 1999276176-A/107.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Koichi,I.
  TITLE     Method for amplifying DNA fragment, method for estimating state of
            microorganism existing and method for estimating state of waste
  JOURNAL   Patent: JP 1999276176-A 107 12-OCT-1999;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
COMMENT     OS   Unidentified
            PN   JP 1999276176-A/107
            PD   12-OCT-1999
            PF   31-MAR-1998 JP 1998087652
            PR
            PI   KOICHI INOUE
            PC   C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC
            Strandedness: Single;
            FH   Key              Location/Qualifiers
            FT   source           1. .12
            FT                    /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match            30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           7 CTACGTGTAC 16
               || |||||||
Db          12 CTTCGTGTAC 3


RESULT 165
E38733/c
LOCUS       E38733                    12 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method and device for amplifying DNA fragment.
ACCESSION   E38733
VERSION     E38733.1  GI:18621395
KEYWORDS    JP 2000270867-A/107.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Inoue,K.
  TITLE     Method and device for amplifying DNA fragment
  JOURNAL   Patent: JP 2000270867-A 107 03-OCT-2000;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
COMMENT     OS   Unidentified
            PN   JP 2000270867-A/107
            PD   03-OCT-2000
            PF   19-MAR-1999 JP 1999076844
            PR
            PI   KOICHI INOUE
            PC   C12N15/09,C12M1/00,C12Q1/68,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key              Location/Qualifiers
            FT   source           1. .12
            FT                    /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match            30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           7 CTACGTGTAC 16
               || |||||||
Db          12 CTTCGTGTAC 3


RESULT 166
E64159/c
LOCUS       E64159                    12 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for amplifying DNA fragment, amplification apparatus of DNA
            fragment, method for assaying a group of microorganisms, method
            for analyzing a group of microorganisms, and method for assaying
            contaminating substance.
ACCESSION   E64159
VERSION     E64159.1  GI:13019563
KEYWORDS    JP 1999341989-A/107.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Koichi,I.
  TITLE     Method for amplifying DNA fragment, amplification apparatus of DNA
            fragment, method for assaying a group of microorganisms, method for
            analyzing a group of microorganisms, and method for assaying
            contaminating substance
  JOURNAL   Patent: JP 1999341989-A 107 14-DEC-1999;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
COMMENT     OS   Artificial Sequence
            PN   JP 1999341989-A/107
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            PD   14-DEC-1999
            PF   16-MAR-1999 JP 1999069694
            PR
            PI   KOICHI INOUE
            PC   C12N15/09,C12M1/00,C12Q1/68,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTAC 16
              || |||||||
Db         12 CTTCGTGTAC 3


RESULT 167
AR205443
LOCUS       AR205443                 12 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 25 from patent US 6368861.
ACCESSION   AR205443
VERSION     AR205443.1  GI:21503026
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Crameri,A., Stemmer,W.P.C., Minshull,J., Bass,S.H., Welch,M.,
            Ness,J.E., Gustafsson,C. and Patten,P.A.
  TITLE     Oligonucleotide mediated nucleic acid recombination
  JOURNAL   Patent: US 6368861-A 25 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              ||| ||||||
Db          2 GGGGGTCCAG 11


RESULT 168
AR220135
LOCUS       AR220135                 12 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 25 from patent US 6423542.
ACCESSION   AR220135
VERSION     AR220135.1  GI:23324577
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Crameri,A., Stemmer,W.P.C., Minshull,J., Bass,S.H., Welch,M.,
            Ness,J.E., Gustafsson,C. and Patten,P.A.
  TITLE     Oligonucleotide mediated nucleic acid recombination
  JOURNAL   Patent: US 6423542-A 25 23-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              ||| ||||||
Db          2 GGGGGTCCAG 11


RESULT 169
AR221524
LOCUS       AR221524                 12 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 25 from patent US 6426224.
ACCESSION   AR221524
VERSION     AR221524.1  GI:23328574
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Crameri,A., Stemmer,W.P.C., Minshull,J., Bass,S.H., Welch,M.,
            Ness,J.E., Gustafsson,C. and Patten,P.A.
  TITLE     Oligonucleotide mediated nucleic acid recombination
  JOURNAL   Patent: US 6426224-A 25 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              ||| ||||||
Db          2 GGGGGTCCAG 11


RESULT 170
AR224308
LOCUS       AR224308                 12 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 39 from patent US 6440719.
ACCESSION   AR224308
VERSION     AR224308.1  GI:23333085
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Draper,K.G.
  TITLE     Method and reagent for inhibiting herpes simplex virus replication
  JOURNAL   Patent: US 6440719-A 39 27-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGT 14
              ||| ||||||
Db          1 CCCGACGTGT 10


RESULT 171
AR254226
LOCUS       AR254226                 12 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 25 from patent US 6479652.
ACCESSION   AR254226
VERSION     AR254226.1  GI:27302963
KEYWORDS    .
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Crameri,A., Stemmer,W.P.C., Minshull,J., Bass,S.H., Welch,M.,
            Ness,J.E., Gustafsson,C. and Patten,P.A.
  TITLE     Oligonucleotide mediated nucleic acid recombination
  JOURNAL   Patent: US 6479652-A 25 12-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              ||| ||||||
Db          2 GGGGGTCCAG 11


RESULT 172
AR282432
LOCUS       AR282432                  12 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 25 from patent US 6521453.
ACCESSION   AR282432
VERSION     AR282432.1  GI:29718588
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Crameri,A., Stemmer,W.P.C., Minshull,J., Bass,S.H., Welch,M.,
            Ness,J.E., Gustafsson,C. and Patten,P.A.
  TITLE     Oligonucloetide mediated nucleic acid recombination
  JOURNAL   Patent: US 6521453-A 25 18-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              ||| ||||||
Db          2 GGGGGTCCAG 11


RESULT 173
AR368339
LOCUS       AR368339                  12 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 25 from patent US 6376246.
ACCESSION   AR368339
VERSION     AR368339.1  GI:34602023
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Crameri,A., Stemmer,W.P.C., Minshull,J., Bass,S.H., Welch,M.,
            Ness,J.E., Gustafsson,C. and Patten,P.A.
  TITLE     Oligonucleotide mediated nucleic acid recombination
  JOURNAL   Patent: US 6376246-A 25 23-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              ||| ||||||
Db          2 GGGGGTCCAG 11


RESULT 174
AX463121/c
LOCUS       AX463121                  12 bp    DNA     linear   PAT 15-JUL-2002
DEFINITION  Sequence 4 from Patent WO0250108.
ACCESSION   AX463121
VERSION     AX463121.1  GI:21886102
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Marchal,G., Pescher,P. and Romain,F.
  TITLE     Immunogenic glycopeptides, screening, preparation and uses
  JOURNAL   Patent: WO 0250108-A 4 27-JUN-2002;
            PASTEUR INSTITUT (FR)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGT 12
              ||||| ||||
Db         12 GGCCCAACGT 3


RESULT 175
AX711090
LOCUS       AX711090                  12 bp    RNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 390 from Patent EP1288296.
ACCESSION   AX711090
VERSION     AX711090.1  GI:29787471
KEYWORDS    .
SOURCE      Herpes simplex virus unknown type
  ORGANISM  Herpes simplex virus unknown type
            Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
            Alphaherpesvirinae; Simplexvirus.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 390 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Herpes simplex virus unknown type"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:126283"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGT 14
              ||| ||||||
Db          1 CCCGACGTGT 10


RESULT 176
BD001193
LOCUS       BD001193                  12 bp    RNA     linear   PAT 31-JAN-2002
DEFINITION  Method and reagent for inhibiting viral replication.
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ACCESSION   BD001193
VERSION     BD001193.1  GI:18625752
KEYWORDS    JP 2000342285-A/353.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
            Holesek,J.J. and Mamone,A.J.
  TITLE     Method and reagent for inhibiting viral replication
  JOURNAL   Patent: JP 2000342285-A 353 12-DEC-2000;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000342285-A/353
            PD   12-DEC-2000
            PF   01-MAY-2000 JP 2000132616
            PR   11-MAY-1992 US    07/882689,14-MAY-1992 US    07/882712 PR
            14-MAY-1992 US    07/882713,14-MAY-1992 US    07/882714 PR
            14-MAY-1992 US    07/882823,14-MAY-1992 US    07/882824 PR
            14-MAY-1992 US    07/882886,14-MAY-1992 US    07/882888 PR
            14-MAY-1992 US    07/882889,14-MAY-1992 US    07/882921 PR
            14-MAY-1992 US    07/882922,14-MAY-1992 US    07/883823 PR
            14-MAY-1992 US    07/883849,14-MAY-1992 US    07/884073 PR
            14-MAY-1992 US    07/884074,14-MAY-1992 US    07/884333 PR
            14-MAY-1992 US    07/884422,14-MAY-1992 US    07/884431 PR
            14-MAY-1992 US    07/884436,14-MAY-1992 US    07/884521 PR
            31-JUL-1992 US    07/923738,26-AUG-1992 US    07/935854 PR
            26-AUG-1992 US    07/936086,18-SEP-1992 US    07/948359 PR
            15-OCT-1992 US    07/963322,07-DEC-1992 US    07/987129 PR
            07-DEC-1992 US    07/987130,07-DEC-1992 US    07/987133 PI
            KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN, PI   DENNIS G
            MAYSEJAK,
            PI   JAMES J HOLESEK,ANTHONY J MAMONE
            PC   C12N15/09,C12N5/10,C12N7/00,C12N9/22//(C12N5/10,C12R1:91), PC
             C12N15/00,
            PC   C12N5/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGT 14
              ||| ||||||
Db          1 CCCGACGTGT 10


RESULT 177
BD001622
LOCUS       BD001622                 12 bp    RNA     linear   PAT 31-JAN-2002
DEFINITION  Method and reagent for inhibiting viral replication.
ACCESSION   BD001622
VERSION     BD001622.1  GI:18626181
KEYWORDS    JP 2000342286-A/353.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
            Holesek,J.J. and Mamone,A.J.
  TITLE     Method and reagent for inhibiting viral replication
  JOURNAL   Patent: JP 2000342286-A 353 12-DEC-2000;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000342286-A/353
            PD   12-DEC-2000
            PF   01-MAY-2000 JP 2000132651
            PR   11-MAY-1992 US    07/882689,14-MAY-1992 US    07/882712 PR
            14-MAY-1992 US    07/882713,14-MAY-1992 US    07/882714 PR
            14-MAY-1992 US    07/882823,14-MAY-1992 US    07/882824 PR
            14-MAY-1992 US    07/882886,14-MAY-1992 US    07/882888 PR
            14-MAY-1992 US    07/882889,14-MAY-1992 US    07/882921 PR
            14-MAY-1992 US    07/882922,14-MAY-1992 US    07/883823 PR
            14-MAY-1992 US    07/883849,14-MAY-1992 US    07/884073 PR
            14-MAY-1992 US    07/884074,14-MAY-1992 US    07/884333 PR
            14-MAY-1992 US    07/884422,14-MAY-1992 US    07/884431 PR
            14-MAY-1992 US    07/884436,14-MAY-1992 US    07/884521 PR
            31-JUL-1992 US    07/923738,26-AUG-1992 US    07/935854 PR
            26-AUG-1992 US    07/936086,18-SEP-1992 US    07/948359 PR
            15-OCT-1992 US    07/963322,07-DEC-1992 US    07/987129 PR
            07-DEC-1992 US    07/987130,07-DEC-1992 US    07/987133 PI
            KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN, PI   DENNIS G
            MAYSEJAK,
            PI   JAMES J HOLESEK,ANTHONY J MAMONE
            PC   C12N15/09,C12N5/10,C12N7/00//A61K38/43,A61K39/125,A61K39/13,
            PC   A61K39/135,
            PC   A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
            PC   A61P1/16,
            PC   A61P31/14,A61P31/16,A61P31/18,A61P31/22,A61P35/02,C12Q1/68, PC
              (C12N15/09,C12R1:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00, PC
             C12R1:93)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGT 14
              ||| ||||||
Db          1 CCCGACGTGT 10


RESULT 178
AR165205/c
LOCUS       AR165205                 21 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 19 from patent US 6274708.
ACCESSION   AR165205
VERSION     AR165205.1  GI:16238680
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Hilton,D.James.
  TITLE     Mouse interleukin-11 receptor
  JOURNAL   Patent: US 6274708-A 19 14-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             29.3%;  Score 8.2;  DB 1;  Length 21;
  Best Local Similarity   76.9%;  Pred. No. 2.8e+02;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGG 19
              || |  |||||||
Db         15 CTCCAAGTACAGG 3
```

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RESULT 179
AX456625/c
LOCUS       AX456625                  9 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 97 from Patent WO0218407.
ACCESSION   AX456625
VERSION     AX456625.1  GI:21715512
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Kurreck,J. and Erdmann,V.A.
  TITLE     Antisense oligonucleotides against vr1
  JOURNAL   Patent: WO 0218407-A 97 07-MAR-2002;
            Gruenenthal GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"

  Query Match             28.6%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCA 26
              ||||||||
Db          9 GGAGTCCA 2


RESULT 180
AX668649/c
LOCUS       AX668649                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2098 from Patent WO0242459.
ACCESSION   AX668649
VERSION     AX668649.1  GI:29291624
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2098 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match             28.6%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCCTACGT 12
              ||||||||
Db          9 CCCTACGT 2


RESULT 181
AX668651/c
LOCUS       AX668651                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2100 from Patent WO0242459.
ACCESSION   AX668651
VERSION     AX668651.1  GI:29291626
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2100 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match             28.6%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCCTACGT 12
              ||||||||
Db          9 CCCTACGT 2


RESULT 182
AX668746
LOCUS       AX668746                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2195 from Patent WO0242459.
ACCESSION   AX668746
VERSION     AX668746.1  GI:29291721
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2195 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match             28.6%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTC 24
              ||||||||
Db          2 AGGGAGTC 9


RESULT 183
AX669004/c
LOCUS       AX669004                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2453 from Patent WO0242459.
ACCESSION   AX669004
VERSION     AX669004.1  GI:29291981
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2453 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
```

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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match             28.6%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          9 CGGGCCCT 2


RESULT 184
AX669005/c
LOCUS       AX669005                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2454 from Patent WO0242459.
ACCESSION   AX669005
VERSION     AX669005.1  GI:29291982
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2454 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match             28.6%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          9 CGGGCCCT 2


RESULT 185
A78814
LOCUS       A78814                   10 bp    DNA     linear   PAT 19-OCT-1999
DEFINITION  Sequence 12 from Patent EP0561245.
ACCESSION   A78814
VERSION     A78814.1  GI:6090408
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hoffman,S.J. and Nagai,K.
  TITLE     BLOOD SUBSTITUTES COMPRISING RECOMBINANT HEMOGLOBIN
  JOURNAL   Patent: EP 0561245-A 12 22-SEP-1993;
            SOMATOGENETICS INT (US); MEDICAL RES COUNCIL (GB)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          3 CGGGCCCT 10


RESULT 186
BD238631
LOCUS       BD238631                 10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD238631
VERSION     BD238631.1  GI:33048401
KEYWORDS    JP 2002534056-A/49.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 49 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/49
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 CCTACGTG 13
              ||||||||
Db          2 CCTACGTG 9


RESULT 187
BD240218
LOCUS       BD240218                 10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD240218
VERSION     BD240218.1  GI:33049988
KEYWORDS    JP 2002534056-A/1636.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1636 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1636
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          3 CGGGCCCT 10


RESULT 188
BD242821/c
LOCUS       BD242821                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Microassay for continuous analysis of gene expression and its
            application.
ACCESSION   BD242821
VERSION     BD242821.1  GI:33052591
KEYWORDS    JP 2002535012-A/11.
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Cheval,L., Elalouf,J.M. and Virlon,B.
  TITLE     Microassay for continuous analysis of gene expression and its
            application
  JOURNAL   Patent: JP 2002535012-A 11 22-OCT-2002;
            COMMISSARIAT A L'ENERGIE ATOMIQUE, CENTRE NATIONAL DE LA RECHERCHE
            SCIENTIFIQUE
COMMENT     OS   Mus sp. (mouse)
            PN   JP 2002535012-A/11
            PD   22-OCT-2002
            PF   25-JAN-2000 JP 2000596176
            PR   27-JAN-1999 EP    99400189.9
            PI   LYDIE CHEVAL,JEAN MARC ELALOUF,BERANGERE VIRLON PC
            C12N15/09,C12Q1/68,C12N15/00
            CC   Microassay for continuous analysis of gene expression and its
            CC             application
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Mus sp. (mouse)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Mus sp."
                      /mol_type="genomic DNA"
                      /db_xref="taxon:10095"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          17 AGGGAGTC 24
               ||||||||
Db           9 AGGGAGTC 2


RESULT 189
E54660
LOCUS       E54660                    10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human normal liver cell expression genes.
ACCESSION   E54660
VERSION     E54660.1  GI:22556143
KEYWORDS    JP 2001211883-A/12.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human normal liver cell expression genes
  JOURNAL   Patent: JP 2001211883-A 12 07-AUG-2001;
            SCIENCE & TECH AGENCY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001211883-A/12
            PD   07-AUG-2001
            PF   31-JAN-2000 JP 2000023170
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K16/18,C12P21/02,C12N15/00
            CC
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          3 CGGGCCCT 10


RESULT 190
I63091
LOCUS       I63091                    10 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 12 from patent US 5661124.
ACCESSION   I63091
VERSION     I63091.1  GI:2480799
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hoffman,S.J. and Nagai,K.
  TITLE     Blood substitutes
  JOURNAL   Patent: US 5661124-A 12 26-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          3 CGGGCCCT 10


RESULT 191
AR274316/c
LOCUS       AR274316                  10 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 12 from patent US 6506561.
ACCESSION   AR274316
VERSION     AR274316.1  GI:29706762
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Cheval,L., Elalouf,J.-M. and Virlon,B.
  TITLE     Method of obtaining a library of tags capable of defining a
            specific state of a biological sample
  JOURNAL   Patent: US 6506561-A 12 14-JAN-2003;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTC 24
              ||||||||
Db          9 AGGGAGTC 2


RESULT 192
AX033036/c
LOCUS       AX033036                  10 bp    DNA     linear   PAT 21-SEP-2000
DEFINITION  Sequence 11 from Patent EP1024201.
ACCESSION   AX033036
VERSION     AX033036.1  GI:10279939
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Elalouf,J.M., Cheval,L. and Virlon,B.
  TITLE     Microassay for serial analysis of gene expression and applications
            thereof
  JOURNAL   Patent: EP 1024201-A 11 02-AUG-2000;
            COMMISSARIAT ENERGIE ATOMIQUE (FR) ; DE CENTRE NAT (FR)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Mus sp."
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10095"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTC 24
              ||||||||
Db          9 AGGGAGTC 2


RESULT 193
AX104933
LOCUS       AX104933                  10 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 1125 from Patent WO0122972.
ACCESSION   AX104933
VERSION     AX104933.1  GI:13921130
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 1125 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 ACGTGTAC 16
              ||||||||
Db          1 ACGTGTAC 8


RESULT 194
AX152549/c
LOCUS       AX152549                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 464 from Patent WO0138577.
ACCESSION   AX152549
VERSION     AX152549.1  GI:14534200
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 464 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 AGTCCAGG 28
              ||||||||
Db         10 AGTCCAGG 3


RESULT 195
AX152759/c
LOCUS       AX152759                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 674 from Patent WO0138577.
ACCESSION   AX152759
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```
VERSION     AX152759.1  GI:14534410
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 674 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 ACGTGTAC 16
              ||||||||
Db         10 ACGTGTAC 3


RESULT 196
AX153021/c
LOCUS       AX153021                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 936 from Patent WO0138577.
ACCESSION   AX153021
VERSION     AX153021.1  GI:14534672
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 936 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GTGTACAG 18
              ||||||||
Db          9 GTGTACAG 2


RESULT 197
AX301658/c
LOCUS       AX301658                  10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 372 from Patent WO0185941.
ACCESSION   AX301658
VERSION     AX301658.1  GI:17382741
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 372 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 ACGTGTAC 16
              ||||||||
Db         10 ACGTGTAC 3


RESULT 198
AX374632
LOCUS       AX374632                  10 bp    DNA     linear   PAT 01-MAR-2002
DEFINITION  Sequence 53 from Patent WO0210454.
ACCESSION   AX374632
VERSION     AX374632.1  GI:19169529
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Choi,J.Y., Koshy,B., Kliem,S. and Stephens,J.C.
  TITLE     Haplotypes of the alas2 gene
  JOURNAL   Patent: WO 0210454-A 53 07-FEB-2002;
            Genaissance Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 AGTCCAGG 28
              ||||||||
Db          2 AGTCCAGG 9


RESULT 199
BD007893
LOCUS       BD007893                  10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  LPS activated human monocyte expressing genes.
ACCESSION   BD007893
VERSION     BD007893.1  GI:18636266
KEYWORDS    JP 2001069993-A/169.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S. and Suzuki,T.
  TITLE     LPS activated human monocyte expressing genes
  JOURNAL   Patent: JP 2001069993-A 169 21-MAR-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001069993-A/169
            PD   21-MAR-2001
            PF   28-APR-2000 JP 2000131079
            PR
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
            C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
            A61P29/00,
            PC   A61P31/00,C12P21/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers
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           FT   source          1. .10
           FT                   /organism='Homo sapiens (human)'.
FEATURES               Location/Qualifiers
     source            1. .10
                       /organism="Homo sapiens"
                       /mol_type="genomic DNA"
                       /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 CCTACGTG 13
              ||||||||
Db          2 CCTACGTG 9


RESULT 200
BD007921/c
LOCUS       BD007921                  10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  LPS activated human monocyte expressing genes.
ACCESSION   BD007921
VERSION     BD007921.1  GI:18636294
KEYWORDS    JP 2001069993-A/197.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S. and Suzuki,T.
  TITLE     LPS activated human monocyte expressing genes
  JOURNAL   Patent: JP 2001069993-A 197 21-MAR-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001069993-A/197
            PD   21-MAR-2001
            PF   28-APR-2000 JP 2000131079
            PR
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
            C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
            A61P29/00,
            PC   A61P31/00,C12P21/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES               Location/Qualifiers
     source            1. .10
                       /organism="Homo sapiens"
                       /mol_type="genomic DNA"
                       /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 ACGTGTAC 16
              ||||||||
Db         10 ACGTGTAC 3


RESULT 201
BD065273
LOCUS       BD065273                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Characterization of the yeast transcriptome.
ACCESSION   BD065273
VERSION     BD065273.1  GI:22610876
KEYWORDS    JP 2001509017-A/209.
SOURCE      Saccharomyces cerevisiae (baker's yeast)
  ORGANISM  Saccharomyces cerevisiae
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Characterization of the yeast transcriptome
  JOURNAL   Patent: JP 2001509017-A 209 10-JUL-2001;
            THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT     OS   Saccharomyces cerevisiae (yeast)
            PN   JP 2001509017-A/209
            PD   10-JUL-2001
            PF   22-JAN-1998 JP 1998532117
            PR   23-JAN-1997 US    60/035917
            PI   VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
            C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
            Characterization of the yeast transcriptome
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Saccharomyces cerevisiae (yeast)'.
FEATURES               Location/Qualifiers
     source            1. .10
                       /organism="Saccharomyces cerevisiae"
                       /mol_type="genomic DNA"
                       /db_xref="taxon:4932"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 GTACAGGG 20
              ||||||||
Db          1 GTACAGGG 8


RESULT 202
BD083323/c
LOCUS       BD083323                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human matured/activated dendritic cell expression genes.
ACCESSION   BD083323
VERSION     BD083323.1  GI:22628933
KEYWORDS    JP 2001327293-A/244.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
  TITLE     Human matured/activated dendritic cell expression genes
  JOURNAL   Patent: JP 2001327293-A 244 27-NOV-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001327293-A/244
            PD   27-NOV-2001
            PF   22-MAY-2000 JP 2000150562
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI  PI
              NAGAI
            PC   C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers.
FEATURES               Location/Qualifiers
     source            1. .10
                       /organism="Homo sapiens"
                       /mol_type="genomic DNA"
                       /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GTGTACAG 18
              ||||||||
Db          9 GTGTACAG 2


RESULT 203
BD167068
LOCUS       BD167068                  10 bp    DNA     linear   PAT 17-JAN-2003
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```
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD167068
VERSION     BD167068.1  GI:27872880
KEYWORDS    JP 2002209591-A/613.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 613 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/613
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          3 CGGGCCCT 10


RESULT 204
BD167170
LOCUS       BD167170                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD167170
VERSION     BD167170.1  GI:27872982
KEYWORDS    JP 2002209591-A/715.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 715 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/715
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          3 CGGGCCCT 10


RESULT 205
AR282864
LOCUS       AR282864                  11 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 9 from patent US 6524792.
ACCESSION   AR282864
VERSION     AR282864.1  GI:29719666
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Renner,W.A., Orberger,G.H., Koller,D. and Bailey,J.E.
  TITLE     Expression cloning processes for the discovery, characterization
            and isolation of genes encoding polypeptides with a predetermined
            property
  JOURNAL   Patent: US 6524792-A 9 25-FEB-2003;
FEATURES              Location/Qualifiers
     source           1. .11
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          4 CGGGCCCT 11


RESULT 206
AX393110
LOCUS       AX393110                  11 bp    DNA     linear   PAT 23-MAR-2002
DEFINITION  Sequence 40 from Patent WO0210217.
ACCESSION   AX393110
VERSION     AX393110.1  GI:19701160
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   St Croix,B., Kinzler,K.W. and Vogelstein,B.
  TITLE     Endothelial cell expression patterns
  JOURNAL   Patent: WO 0210217-A 40 07-FEB-2002;
            The Johns Hopkins University (US)
FEATURES              Location/Qualifiers
     source           1. .11
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GGCCCTAC 10
              ||||||||
Db          1 GGCCCTAC 8


RESULT 207
AX421267
```

```
LOCUS       AX421267                 11 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 15 from Patent WO0218641.
ACCESSION   AX421267
VERSION     AX421267.1  GI:21524675
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Risinger,C., Andersson,M.K., Lewander,T. and Olaisson,E.
  TITLE     Detection of cyp3a4 and cyp2c9 polymorphisms
  JOURNAL   Patent: WO 0218641-A 15 07-MAR-2002;
            Gemini Genomics PLC (GB)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide of the novel polymorphic site 461
                     on the coding strand"

  Query Match           28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 GTGTACAG 18
               ||||||||
Db           3 GTGTACAG 10


RESULT 208
AX421268/c
LOCUS       AX421268                 11 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 16 from Patent WO0218641.
ACCESSION   AX421268
VERSION     AX421268.1  GI:21524676
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Risinger,C., Andersson,M.K., Lewander,T. and Olaisson,E.
  TITLE     Detection of cyp3a4 and cyp2c9 polymorphisms
  JOURNAL   Patent: WO 0218641-A 16 07-MAR-2002;
            Gemini Genomics PLC (GB)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide of the novel polymorphic site 461
                     on the non-coding strand"

  Query Match           28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 GTGTACAG 18
               ||||||||
Db           9 GTGTACAG 2


RESULT 209
AX470469/c
LOCUS       AX470469                 11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 46 from Patent WO02053773.
ACCESSION   AX470469
VERSION     AX470469.1  GI:22205594
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 46 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          21 AGTCCAGG 28
               ||||||||
Db          10 AGTCCAGG 3


RESULT 210
AX470788
LOCUS       AX470788                 11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 365 from Patent WO02053773.
ACCESSION   AX470788
VERSION     AX470788.1  GI:22205913
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 365 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          19 GGAGTCCA 26
               ||||||||
Db           2 GGAGTCCA 9


RESULT 211
AX470933/c
LOCUS       AX470933                 11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 510 from Patent WO02053773.
ACCESSION   AX470933
VERSION     AX470933.1  GI:22206058
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 510 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GAGTCCAG 27
              ||||||||
Db         11 GAGTCCAG 4


RESULT 212
AX471363
LOCUS       AX471363                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 940 from Patent WO02053773.
ACCESSION   AX471363
VERSION     AX471363.1  GI:22206488
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 940 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCC 25
              ||||||||
Db          4 GGGAGTCC 11


RESULT 213
AX471851
LOCUS       AX471851                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 1428 from Patent WO02053773.
ACCESSION   AX471851
VERSION     AX471851.1  GI:22206976
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 1428 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCA 26
              ||||||||
Db          3 GGAGTCCA 10


RESULT 214
AX623060
LOCUS       AX623060                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 101 from Patent WO02053774.
ACCESSION   AX623060
VERSION     AX623060.1  GI:28451001
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 101 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAG 22
              ||||||||
Db          2 ACAGGGAG 9


RESULT 215
AX623555/c
LOCUS       AX623555                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 596 from Patent WO02053774.
ACCESSION   AX623555
VERSION     AX623555.1  GI:28451496
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 596 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 AGTCCAGG 28
              ||||||||
Db         11 AGTCCAGG 4


RESULT 216
AX624143
LOCUS       AX624143                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 1184 from Patent WO02053774.
ACCESSION   AX624143
VERSION     AX624143.1  GI:28452084
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
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  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 1184 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TGTACAGG 19
              ||||||||
Db          4 TGTACAGG 11


RESULT 217
AX625138/c
LOCUS       AX625138                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2179 from Patent WO02053774.
ACCESSION   AX625138
VERSION     AX625138.1  GI:28453079
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2179 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GAGTCCAG 27
              ||||||||
Db         11 GAGTCCAG 4


RESULT 218
AX625188/c
LOCUS       AX625188                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2229 from Patent WO02053774.
ACCESSION   AX625188
VERSION     AX625188.1  GI:28453129
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2229 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CTACGTGT 14
              ||||||||
Db         11 CTACGTGT 4


RESULT 219
AX625450
LOCUS       AX625450                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2491 from Patent WO02053774.
ACCESSION   AX625450
VERSION     AX625450.1  GI:28453391
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2491 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GCCCTACG 11
              ||||||||
Db          4 GCCCTACG 11


RESULT 220
AX625464/c
LOCUS       AX625464                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2505 from Patent WO02053774.
ACCESSION   AX625464
VERSION     AX625464.1  GI:28453405
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2505 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GGGCCCTA 9
              ||||||||
Db          9 GGGCCCTA 2


RESULT 221
AX625855
LOCUS       AX625855                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2896 from Patent WO02053774.
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ACCESSION   AX625855
VERSION     AX625855.1  GI:28453893
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2896 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          20 GAGTCCAG 27
               ||||||||
Db           4 GAGTCCAG 11


RESULT 222
AX626664
LOCUS       AX626664                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3705 from Patent WO02053774.
ACCESSION   AX626664
VERSION     AX626664.1  GI:28454702
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3705 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          18 GGGAGTCC 25
               ||||||||
Db           4 GGGAGTCC 11


RESULT 223
AX627013
LOCUS       AX627013                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4054 from Patent WO02053774.
ACCESSION   AX627013
VERSION     AX627013.1  GI:28455051
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4054 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           2 GGGCCCTA 9
               ||||||||
Db           3 GGGCCCTA 10


RESULT 224
AX627782/c
LOCUS       AX627782                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4823 from Patent WO02053774.
ACCESSION   AX627782
VERSION     AX627782.1  GI:28455820
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4823 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          21 AGTCCAGG 28
               ||||||||
Db          10 AGTCCAGG 3


RESULT 225
AX629261/c
LOCUS       AX629261                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6302 from Patent WO02053774.
ACCESSION   AX629261
VERSION     AX629261.1  GI:28457299
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6302 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          15 ACAGGGAG 22
               ||||||||
Db          11 ACAGGGAG 4


RESULT 226
AX629639
LOCUS       AX629639                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6680 from Patent WO02053774.
ACCESSION   AX629639
VERSION     AX629639.1  GI:28457677
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6680 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          19 GGAGTCCA 26
               ||||||||
Db           2 GGAGTCCA 9


RESULT 227
AX629743/c
LOCUS       AX629743                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6784 from Patent WO02053774.
ACCESSION   AX629743
VERSION     AX629743.1  GI:28457781
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6784 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          20 GAGTCCAG 27
               ||||||||
Db           9 GAGTCCAG 2


RESULT 228
AX630481
LOCUS       AX630481                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7522 from Patent WO02053774.
ACCESSION   AX630481
VERSION     AX630481.1  GI:28458519
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7522 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          15 ACAGGGAG 22
               ||||||||
Db           2 ACAGGGAG 9


RESULT 229
AX630976/c
LOCUS       AX630976                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 8017 from Patent WO02053774.
ACCESSION   AX630976
VERSION     AX630976.1  GI:28459018
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8017 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          21 AGTCCAGG 28
               ||||||||
Db          11 AGTCCAGG 4


RESULT 230
AX631564
LOCUS       AX631564                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 8606 from Patent WO02053774.
ACCESSION   AX631564
VERSION     AX631564.1  GI:28459640
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8606 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
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     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TGTACAGG 19
              ||||||||
Db          4 TGTACAGG 11


RESULT 231
AX632559/c
LOCUS       AX632559                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9601 from Patent WO02053774.
ACCESSION   AX632559
VERSION     AX632559.1  GI:28468174
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9601 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GAGTCCAG 27
              ||||||||
Db         11 GAGTCCAG 4


RESULT 232
AX632609/c
LOCUS       AX632609                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9651 from Patent WO02053774.
ACCESSION   AX632609
VERSION     AX632609.1  GI:28468224
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9651 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CTACGTGT 14
              ||||||||
Db         11 CTACGTGT 4


RESULT 233
AX632794
LOCUS       AX632794                 11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9836 from Patent WO02053774.
ACCESSION   AX632794
VERSION     AX632794.1  GI:28468409
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9836 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             28.6%;  Score 8;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCA 26
              ||||||||
Db          3 GGAGTCCA 10


RESULT 234
I11566
LOCUS       I11566                   12 bp    DNA     linear   PAT 26-JUL-1995
DEFINITION  Sequence 4 from Patent US 5407822.
ACCESSION   I11566
VERSION     I11566.1  GI:909084
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Leplatois,P., Loison,G., Pessegue,B. and Shire,D.
  TITLE     Artificial promoter for the expression of proteins in yeast
  JOURNAL   Patent: US 5407822-A 4 18-APR-1995;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          5 CGGGCCCT 12


RESULT 235
I14185
LOCUS       I14185                   12 bp    DNA     linear   PAT 26-SEP-1995
DEFINITION  Sequence 17 from patent US 5446138.
ACCESSION   I14185
VERSION     I14185.1  GI:996608
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
```

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  AUTHORS   Blaiseu,P.-L., Legoux,R., Leguay,J.-J. and Schneider,M.
  TITLE     Recombinant DNA coding for a protein with endochitinase activity
  JOURNAL   Patent: US 5446138-A 17 29-AUG-1995;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match           28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          5 CGGGCCCT 12


RESULT 236
I24587/c
LOCUS       I24587                    12 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 15 from patent US 5545526.
ACCESSION   I24587
VERSION     I24587.1  GI:1604457
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Baxter-Lowe,L.Ann.
  TITLE     Method for HLA Typing
  JOURNAL   Patent: US 5545526-A 15 13-AUG-1996;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match           28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          9 CGGGCCCT 2


RESULT 237
AX235321
LOCUS       AX235321                  12 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 23 from Patent WO0162967.
ACCESSION   AX235321
VERSION     AX235321.1  GI:15593866
KEYWORDS    .
SOURCE      Hordeum vulgare
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1
  AUTHORS   Vider,B.Z. and Katzir,N.
  TITLE     A method that compares genomic sequences
  JOURNAL   Patent: WO 0162967-A 23 30-AUG-2001;
            Genena Ltd. (IL) ; Agricultural Research Organization Newe Ya'Ar
            Research Center (IL)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Hordeum vulgare"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:4513"

  Query Match           28.6%;  Score 8;  DB 1;  Length 12;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 CCTACGTG 13
              ||||||||
Db          1 CCTACGTG 8


RESULT 238
AX711182
LOCUS       AX711182                  17 bp    DNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 482 from Patent EP1288296.
ACCESSION   AX711182
VERSION     AX711182.1  GI:29787563
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 482 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic acid clone fragments"

  Query Match           28.6%;  Score 8;  DB 1;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 2.6e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          7 CGGGCCCT 14


RESULT 239
AX625951
LOCUS       AX625951                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2992 from Patent WO02053774.
ACCESSION   AX625951
VERSION     AX625951.1  GI:28453989
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2992 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity  81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || | ||||||
Db          1 CTTCCTGTACA 11


RESULT 240
AX472098/c
LOCUS       AX472098                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 89 from Patent WO02053775.
ACCESSION   AX472098
```

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VERSION     AX472098.1  GI:22207139
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hustert,E., Haberl,M. and Wojnowski,L.
  TITLE     Identification of the genetic determinants of the polymorphic
            cyp3a5 expression
  JOURNAL   Patent: WO 02053775-A 89 11-JUL-2002;
            EPIDAUROS BIOTECHNOLOGIE AG (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTAC 16
              ||| | |||||
Db         11 CCTTCCTGTAC 1


RESULT 241
I16095
LOCUS       I16095                    11 bp    DNA     linear   PAT 03-APR-1996
DEFINITION  Sequence 4 from patent US 5474897.
ACCESSION   I16095
VERSION     I16095.1  GI:1251003
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Weiss,A. and Fraser,J.
  TITLE     Screening assay for the identification ov novel immunosuppressives
            using cultured T cells
  JOURNAL   Patent: US 5474897-A 4 12-DEC-1995;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCCA 26
              ||| || ||||
Db          1 CAGAGATTCCA 11


RESULT 242
AR301655
LOCUS       AR301655                  11 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 236 from patent US 6538173.
ACCESSION   AR301655
VERSION     AR301655.1  GI:31689457
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Heber-Katz,E.
  TITLE     Compositions and methods for wound healing
  JOURNAL   Patent: US 6538173-A 236 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAGG 28
              ||| | |||||
Db          1 GGGGGCCCAGG 11


RESULT 243
AR301691/c
LOCUS       AR301691                  11 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 272 from patent US 6538173.
ACCESSION   AR301691
VERSION     AR301691.1  GI:31689493
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Heber-Katz,E.
  TITLE     Compositions and methods for wound healing
  JOURNAL   Patent: US 6538173-A 272 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGG 20
              | |||| ||||
Db         11 CTTGTAGAGGG 1


RESULT 244
AX470747/c
LOCUS       AX470747                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 324 from Patent WO02053773.
ACCESSION   AX470747
VERSION     AX470747.1  GI:22205872
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 324 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCCA 26
              ||| ||| |||
Db         11 CAGAGAGGCCA 1


RESULT 245
AX470906/c
LOCUS       AX470906                  11 bp    DNA     linear   PAT 09-AUG-2002
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```
DEFINITION  Sequence 483 from Patent WO02053773.
ACCESSION   AX470906
VERSION     AX470906.1  GI:22206031
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 483 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GGGCCCTACGT 12
              |||||||  || .
Db         11 GGGCCCTTTGT 1


RESULT 246
AX470952/c
LOCUS       AX470952                 11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 529 from Patent WO02053773.
ACCESSION   AX470952
VERSION     AX470952.1  GI:22206077
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 529 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCCA 26
              | ||| |||||
Db         11 CGGGGGGTCCA 1


RESULT 247
AX471524
LOCUS       AX471524                 11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 1101 from Patent WO02053773.
ACCESSION   AX471524
VERSION     AX471524.1  GI:22206649
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 1101 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGA 21
              ||||| | |||
Db          1 GTGTAAATGGA 11


RESULT 248
AX471669/c
LOCUS       AX471669                 11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 1246 from Patent WO02053773.
ACCESSION   AX471669
VERSION     AX471669.1  GI:22206794
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 1246 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAGG 28
              |||| | ||||
Db         11 GGGACTGCAGG 1


RESULT 249
AX471699/c
LOCUS       AX471699                 11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 1276 from Patent WO02053773.
ACCESSION   AX471699
VERSION     AX471699.1  GI:22206824
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 1276 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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```
Qy          5 CCCTACGTGTA 15
              ||  |||||||
Db         11 CCTCACGTGTA 1


RESULT 250
AX471796/c
LOCUS       AX471796                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 1373 from Patent WO02053773.
ACCESSION   AX471796
VERSION     AX471796.1  GI:22206921
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 1373 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCCA 26
              | |||||  |||
Db         11 CGGGGAGGCCA 1


RESULT 251
AX623640/c
LOCUS       AX623640                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 681 from Patent WO02053774.
ACCESSION   AX623640
VERSION     AX623640.1  GI:28451581
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 681 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAGG 28
              |||| ||  |||
Db         11 GGGATTCTAGG 1


RESULT 252
AX624024/c
LOCUS       AX624024                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 1065 from Patent WO02053774.
ACCESSION   AX624024
VERSION     AX624024.1  GI:28451965
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 1065 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAGG 28
              |||| | ||||
Db         11 GGGATTTCAGG 1


RESULT 253
AX624330/c
LOCUS       AX624330                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 1371 from Patent WO02053774.
ACCESSION   AX624330
VERSION     AX624330.1  GI:28452271
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 1371 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAGG 28
              |||| | ||||
Db         11 GGGATTGCAGG 1


RESULT 254
AX624837/c
LOCUS       AX624837                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 1878 from Patent WO02053774.
ACCESSION   AX624837
VERSION     AX624837.1  GI:28452778
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 1878 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAGG 28
              |||| | ||||
Db         11 GGGAATACAGG 1


RESULT 255
AX625047/c
LOCUS       AX625047                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2088 from Patent WO02053774.
ACCESSION   AX625047
VERSION     AX625047.1  GI:28452988
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2088 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAGG 28
              || || |||||
Db         11 GGTAGGCCAGG 1


RESULT 256
AX625403
LOCUS       AX625403                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2444 from Patent WO02053774.
ACCESSION   AX625403
VERSION     AX625403.1  GI:28453344
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2444 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTCCAG 27
              ||||| || |
Db          1 AGGGAGACCTG 11


RESULT 257
AX625794
LOCUS       AX625794                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2835 from Patent WO02053774.
ACCESSION   AX625794
VERSION     AX625794.1  GI:28453735
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2835 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCCA 26
              |||| || ||
Db          1 CAGGGGGTTCA 11


RESULT 258
AX626034/c
LOCUS       AX626034                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3075 from Patent WO02053774.
ACCESSION   AX626034
VERSION     AX626034.1  GI:28454072
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3075 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCCA 26
              ||| ||| |||
Db         11 CAGAGAGGCCA 1


RESULT 259
AX626752/c
LOCUS       AX626752                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3793 from Patent WO02053774.
ACCESSION   AX626752
VERSION     AX626752.1  GI:28454790
KEYWORDS    .
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3793 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GGGCCCTACGT 12
              |||||||  ||
Db         11 GGGCCCTTTGT 1


RESULT 260
AX626783/c
LOCUS       AX626783                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3824 from Patent WO02053774.
ACCESSION   AX626783
VERSION     AX626783.1  GI:28454821
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3824 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          18 GGGAGTCCAGG 28
               |||  ||||||
Db          11 GGGGTTCCAGG 1


RESULT 261
AX626888
LOCUS       AX626888                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3929 from Patent WO02053774.
ACCESSION   AX626888
VERSION     AX626888.1  GI:28454926
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3929 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          14 TACAGGGAGTC 24
               ||  |||||||
Db           1 TAATGGGAGTC 11


RESULT 262
AX627660
LOCUS       AX627660                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4701 from Patent WO02053774.
ACCESSION   AX627660
VERSION     AX627660.1  GI:28455698
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4701 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          16 CAGGGAGTCCA 26
               ||| || ||||
Db           1 CAGTGATTCCA 11


RESULT 263
AX627965
LOCUS       AX627965                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5006 from Patent WO02053774.
ACCESSION   AX627965
VERSION     AX627965.1  GI:28456003
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5006 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          11 GTGTACAGGGA 21
               ||||| | |||
Db           1 GTGTAAATGGA 11
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RESULT 264
AX628121/c
LOCUS       AX628121                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5162 from Patent WO02053774.
ACCESSION   AX628121
VERSION     AX628121.1  GI:28456159
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5162 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAGG 28
              |||| | ||||
Db         11 GGGACTGCAGG 1


RESULT 265
AX628521/c
LOCUS       AX628521                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5562 from Patent WO02053774.
ACCESSION   AX628521
VERSION     AX628521.1  GI:28456559
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5562 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTCCAG 27
              ||||| || ||
Db         11 AGGGAATCTAG 1


RESULT 266
AX628699/c
LOCUS       AX628699                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5740 from Patent WO02053774.
ACCESSION   AX628699
VERSION     AX628699.1  GI:28456737
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5740 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCCA 26
              | ||| |||||
Db         11 CGGGGGGTCCA 1


RESULT 267
AX629205
LOCUS       AX629205                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6246 from Patent WO02053774.
ACCESSION   AX629205
VERSION     AX629205.1  GI:28457243
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6246 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAGTCC 25
              |||||| | ||
Db          1 ACAGGGTGACC 11


RESULT 268
AX629571
LOCUS       AX629571                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6612 from Patent WO02053774.
ACCESSION   AX629571
VERSION     AX629571.1  GI:28457609
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6612 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GGGCCCTACGT 12
              ||||||| | ||
Db          1 GGGCCCTTCCT 11


RESULT 269
AX629648
LOCUS       AX629648                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6689 from Patent WO02053774.
ACCESSION   AX629648
VERSION     AX629648.1  GI:28457686
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6689 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTA 15
              ||  |||||||
Db          1 CCAAACGTGTA 11


RESULT 270
AX629882/c
LOCUS       AX629882                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6923 from Patent WO02053774.
ACCESSION   AX629882
VERSION     AX629882.1  GI:28457920
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6923 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTA 15
              ||  |||||||
Db         11 CCTCACGTGTA 1


RESULT 271
AX630279
LOCUS       AX630279                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7320 from Patent WO02053774.
ACCESSION   AX630279
VERSION     AX630279.1  GI:28458317
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7320 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAGG 28
              ||||| || ||
Db          1 GGGAGCCCGGG 11


RESULT 272
AX631061/c
LOCUS       AX631061                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 8102 from Patent WO02053774.
ACCESSION   AX631061
VERSION     AX631061.1  GI:28459103
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8102 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAGG 28
              |||| || |||
Db         11 GGGATTCTAGG 1


RESULT 273
AX631445/c
LOCUS       AX631445                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 8487 from Patent WO02053774.
ACCESSION   AX631445
VERSION     AX631445.1  GI:28459511
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8487 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAGG 28
              |||| | ||||
Db         11 GGGATTTCAGG 1


RESULT 274
AX631751/c
LOCUS       AX631751                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 8793 from Patent WO02053774.
ACCESSION   AX631751
VERSION     AX631751.1  GI:28459858
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8793 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAGG 28
              |||| | ||||
Db         11 GGGATTGCAGG 1


RESULT 275
AX632258/c
LOCUS       AX632258                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9300 from Patent WO02053774.
ACCESSION   AX632258
VERSION     AX632258.1  GI:28467873
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9300 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAGG 28
              |||| | ||||
Db         11 GGGAATACAGG 1


RESULT 276
AX632468/c
LOCUS       AX632468                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9510 from Patent WO02053774.
ACCESSION   AX632468
VERSION     AX632468.1  GI:28468083
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9510 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAGG 28
              || || |||||
Db         11 GGTAGGCCAGG 1


RESULT 277
BD124405
LOCUS       BD124405                  11 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Compositions and method for healing wound.
ACCESSION   BD124405
VERSION     BD124405.1  GI:23219350
KEYWORDS    JP 2002503460-A/236.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Katz,E.H.
  TITLE     Compositions and method for healing wound
  JOURNAL   Patent: JP 2002503460-A 236 05-FEB-2002;
            THE WISTAR INSTITUTE
COMMENT     OS   Mus musculus (mouse)
            PN   JP 2002503460-A/236
            PD   05-FEB-2002
            PF   12-FEB-1999 JP 2000531545
            PR   13-FEB-1998 US    60/074737,26-AUG-1998 US    60/097937 PR
            28-SEP-1998 US    60/102051
            PI   ELLEN HEBER KATZ
            PC   C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
              C12N5/00
            CC   Compositions and method for healing wound
            FH   Key             Location/Qualifiers
            FT   source          1. .11
            FT                   /organism='Mus musculus (mouse)'.
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
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                     /db_xref="taxon:10090"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAGG 28
              ||| | |||||
Db          1 GGGGGCCCAGG 11


RESULT 278
BD124441/c
LOCUS       BD124441                  11 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Compositions and method for healing wound.
ACCESSION   BD124441
VERSION     BD124441.1  GI:23219386
KEYWORDS    JP 2002503460-A/272.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Katz,E.H.
  TITLE     Compositions and method for healing wound
  JOURNAL   Patent: JP 2002503460-A 272 05-FEB-2002;
            THE WISTAR INSTITUTE
COMMENT     OS   Mus musculus (mouse)
            PN   JP 2002503460-A/272
            PD   05-FEB-2002
            PF   12-FEB-1999 JP 2000531545
            PR   13-FEB-1998 US    60/074737,26-AUG-1998 US    60/097937 PR
            28-SEP-1998 US    60/102051
            PI   ELLEN HEBER KATZ
            PC   C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
              C12N5/00
            CC   Compositions and method for healing wound
            FH   Key             Location/Qualifiers
            FT   source          1. .11
            FT                   /organism='Mus musculus (mouse)'.
FEATURES              Location/Qualifiers
     source           1. .11
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:10090"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGG 20
              | |||| ||||
Db         11 CTTGTAGAGGG 1


RESULT 279
A47665/c
LOCUS       A47665                    12 bp    DNA     linear   PAT 07-MAR-1997
DEFINITION  Sequence 25 from Patent EP0692535.
ACCESSION   A47665
VERSION     A47665.1  GI:2301606
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Colote,S. and Pirotzky,E.
  TITLE     Oligonucleotides to inhibit the role of isoprenyl protein
            transferases
  JOURNAL   Patent: EP 0692535-A 25 17-JAN-1996;
            SOD CONSEILS RECH APPLIC (FR)
COMMENT     Other publication CN 1124142 960612
            Other publication CZ 9501688 960515
            Other publication BR 9503015 960604
            Other publication NZ 272398 960426
            Other publication HU 72133 960328
            Other publication JP 8051985 960227
            Other publication FR 2721930 960105
            Other publication FR 2721827 960105
            Other publication FI 953170 951230
            Other publication SE 9502259 951230
            Other publication PL 309384 960108
            Other publication NO 952601 960102
            Other publication AU 2329995 960111
            Other publication CA 2152233 951230
            Other publication GB 2290791 960110.
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="unidentified"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32644"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAGT 23
              || ||| ||||
Db         11 GTCCAGAGAGT 1


RESULT 280
A91496/c
LOCUS       A91496                    12 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 23 from Patent WO9824928.
ACCESSION   A91496
VERSION     A91496.1  GI:6740451
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Pallisgaard,N. and Hokland,P.
  TITLE     DETECTION OF CHROMOSOMAL ABNORMALITIES
  JOURNAL   Patent: WO 9824928-A 23 11-JUN-1998;
            PALLISGAARD NIELS (DK); HOKLAND PETER (DK)
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="unidentified"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32644"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              |||||  ||||
Db         11 CTACGCCTACA 1


RESULT 281
AR027883/c
LOCUS       AR027883                  12 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 25 from patent US 5856461.
ACCESSION   AR027883
VERSION     AR027883.1  GI:5938703
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Colote,S. and Pirotzky,E.
  TITLE     Oligonucleotides to inhibit the expression of isoprenyl protein
            transferases
  JOURNAL   Patent: US 5856461-A 25 05-JAN-1999;
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FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAGT 23
              || ||| ||||
Db         11 GTCCAGAGAGT 1


RESULT 282
AR167661/c
LOCUS       AR167661                  12 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 25 from patent US 6287769.
ACCESSION   AR167661
VERSION     AR167661.1  GI:17903456
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Inoue,T.
  TITLE     Method of amplifying DNA fragment, apparatus for amplifying DNA
            fragment, method of assaying microorganisms, method of analyzing
            microorganisms and method of assaying contaminant
  JOURNAL   Patent: US 6287769-A 25 11-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || |||||| |
Db         11 CTTCGTGTAGA 1


RESULT 283
E29545/c
LOCUS       E29545                    12 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for amplifying DNA fragment, method for estimating state of
            microorganism existing and method for estimating state of waste.
ACCESSION   E29545
VERSION     E29545.1  GI:13021048
KEYWORDS    JP 1999276176-A/25.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Koichi,I.
  TITLE     Method for amplifying DNA fragment, method for estimating state of
            microorganism existing and method for estimating state of waste
  JOURNAL   Patent: JP 1999276176-A 25 12-OCT-1999;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
COMMENT     OS   Unidentified
            PN   JP 1999276176-A/25
            PD   12-OCT-1999
            PF   31-MAR-1998 JP 1998087652
            PR
            PI   KOICHI INOUE
            PC   C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC
            Strandedness: Single;
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || |||||| |
Db         11 CTTCGTGTAGA 1


RESULT 284
E38651/c
LOCUS       E38651                    12 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method and device for amplifying DNA fragment.
ACCESSION   E38651
VERSION     E38651.1  GI:18621313
KEYWORDS    JP 2000270867-A/25.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Inoue,K.
  TITLE     Method and device for amplifying DNA fragment
  JOURNAL   Patent: JP 2000270867-A 25 03-OCT-2000;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
COMMENT     OS   Unidentified
            PN   JP 2000270867-A/25
            PD   03-OCT-2000
            PF   19-MAR-1999 JP 1999076844
            PR
            PI   KOICHI INOUE
            PC   C12N15/09,C12M1/00,C12Q1/68,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || |||||| |
Db         11 CTTCGTGTAGA 1


RESULT 285
E64077/c
LOCUS       E64077                    12 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for amplifying DNA fragment, amplification apparatus of DNA
            fragment, method for assaying a group of microorganisms, method
            for analyzing a group of microorganisms, and method for assaying
            contaminating substance.
ACCESSION   E64077
VERSION     E64077.1  GI:13019481
KEYWORDS    JP 1999341989-A/25.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Koichi,I.
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```
  TITLE     Method for amplifying DNA fragment, amplification apparatus of DNA
            fragment, method for assaying a group of microorganisms, method for
            analyzing a group of microorganisms, and method for assaying
            contaminating substance
  JOURNAL   Patent: JP 1999341989-A 25 14-DEC-1999;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
COMMENT     OS   Artificial Sequence
            PN   JP 1999341989-A/25
            PD   14-DEC-1999
            PF   16-MAR-1999 JP 1999069694
            PR
            PI   KOICHI INOUE
            PC   C12N15/09,C12M1/00,C12Q1/68,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              || |||||| |
Db         11 CTTCGTGTAGA 1


RESULT 286
I23754/c
LOCUS       I23754                  12 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 19 from patent US 5538844.
ACCESSION   I23754
VERSION     I23754.1  GI:1603624
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Duyao,M.P., MacDonald,M.E. and Gusella,J.F.
  TITLE     Transport protein gene from the Huntington's disease region
  JOURNAL   Patent: US 5538844-A 19 23-JUL-1996;
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTA 15
              |||||| || |
Db         12 CCCTACCTGAA 2


RESULT 287
I35021/c
LOCUS       I35021                  12 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 107 from patent US 5599704.
ACCESSION   I35021
VERSION     I35021.1  GI:2087989
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Thompson,J.D. and Draper,K.G.
  TITLE     ErbB2/neu targeted ribozymes
  JOURNAL   Patent: US 5599704-A 107 04-FEB-1997;
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGT 14
              ||| || ||||
Db         12 GCCGTAGGTGT 2


RESULT 288
AR224412
LOCUS       AR224412                12 bp    RNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 9 from patent US 6440723.
ACCESSION   AR224412
VERSION     AR224412.1  GI:23333191
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Dale,R.M.K.
  TITLE     Arrays with modified oligonucleotide and polynucleotide
            compositions
  JOURNAL   Patent: US 6440723-A 9 27-AUG-2002;
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="unknown"
                      /mol_type="unassigned RNA"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAGTCC 25
              | |||||  |||
Db          1 ATAGGGAATCC 11


RESULT 289
AX073604/c
LOCUS       AX073604                12 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 26 from Patent WO0104320.
ACCESSION   AX073604
VERSION     AX073604.1  GI:12710027
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Schmidt,A.C., Skiadopoulos,M.H., Collins,P.L., Murphy,B.R.,
            Bailly,J.E. and Durbin,A.P.
  TITLE     Attenuated human-bovine chimeric parainfluenza virus (piv) vaccines
  JOURNAL   Patent: WO 0104320-A 26 18-JAN-2001;
            THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Sequence flanking site for introduction of Bsi W1
                      site for rHPIV3 s"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy          5 CCCTACGTGTA 15
              || ||||| ||
Db         11 CCGTACGTCTA 1


RESULT 290
AX073609/c
LOCUS       AX073609                  12 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 31 from Patent WO0104320.
ACCESSION   AX073609
VERSION     AX073609.1  GI:12710032
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Schmidt,A.C., Skiadopoulos,M.H., Collins,P.L., Murphy,B.R.,
            Bailly,J.E. and Durbin,A.P.
  TITLE     Attenuated human-bovine chimeric parainfluenza virus (piv) vaccines
  JOURNAL   Patent: WO 0104320-A 31 18-JAN-2001;
            THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sequence flanking Bsi W1 site in rBPIV3 of sFHHNH"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTA 15
              || ||||| ||
Db         11 CCGTACGTCTA 1


RESULT 291
AX105625
LOCUS       AX105625                  12 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 9 from Patent WO0123620.
ACCESSION   AX105625
VERSION     AX105625.1  GI:13921655
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dale,R.M.
  TITLE     Arrays with modified oligonucleotide and polynucleotide
            compositions
  JOURNAL   Patent: WO 0123620-A 9 05-APR-2001;
            Oligos Etc. Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthesized oligonucleotide"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAGTCC 25
              | ||||| |||
Db          1 ATAGGGAATCC 11


RESULT 292
AX454105/c
LOCUS       AX454105                  12 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 55 from Patent WO0202605.
ACCESSION   AX454105
VERSION     AX454105.1  GI:21713743
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Skiadopoulos,M.H., Collins,P.L., Murphy,B.R. and Schmidt,A.C.
  TITLE     Attenuated human-bovine chimeric parainfluenza virus (piv) vaccines
  JOURNAL   Patent: WO 0202605-A 55 10-JAN-2002;
            THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Parainfluenza Virus"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTA 15
              || ||||| ||
Db         11 CCGTACGTCTA 1


RESULT 293
AX454110/c
LOCUS       AX454110                  12 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 60 from Patent WO0202605.
ACCESSION   AX454110
VERSION     AX454110.1  GI:21713748
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Skiadopoulos,M.H., Collins,P.L., Murphy,B.R. and Schmidt,A.C.
  TITLE     Attenuated human-bovine chimeric parainfluenza virus (piv) vaccines
  JOURNAL   Patent: WO 0202605-A 60 10-JAN-2002;
            THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Parainfluenza Virus"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTA 15
              || ||||| ||
Db         11 CCGTACGTCTA 1


RESULT 294
BD023278/c
LOCUS       BD023278                  12 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for detecting abnormality in chromosome.
ACCESSION   BD023278
VERSION     BD023278.1  GI:22564501
KEYWORDS    JP 2001505428-A/23.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Parisgard,N. and Hokurando,P.
  TITLE     Method for detecting abnormality in chromosome
  JOURNAL   Patent: JP 2001505428-A 23 24-APR-2001;
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            NEILLS PARISGARD
COMMENT     PN   JP 2001505428-A/23
            PD   24-APR-2001
            PF   08-DEC-1997 JP 1998525090
            PI   NEILLS PARISGARD,PATER HOKURANDO
            PC   C12N15/09,C12Q1/68,G01N33/50,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   /desc = 'DNA (synthetic)'
            FH   Key             Location/Qualifiers.
FEATURES            Location/Qualifiers
     source         1. .12
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"

  Query Match            27.9%;  Score 7.8;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              ||||| ||||
Db         11 CTACGCCTACA 1


RESULT 295
AX690109/c
LOCUS       AX690109                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 2841 from Patent EP1281758.
ACCESSION   AX690109
VERSION     AX690109.1  GI:29412967
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 2841 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES            Location/Qualifiers
     source         1. .25
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"

  Query Match            27.9%;  Score 7.8;  DB 1;  Length 25;
  Best Local Similarity   63.2%;  Pred. No. 2.9e+02;
  Matches   12;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTACAGGGAG 22
              || ||   || ||| | ||
Db         23 GCACTCGCTGCACACGTAG 5


RESULT 296
AX690110/c
LOCUS       AX690110                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 2842 from Patent EP1281758.
ACCESSION   AX690110
VERSION     AX690110.1  GI:29412968
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 2842 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES            Location/Qualifiers
     source         1. .25
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"

  Query Match            27.9%;  Score 7.8;  DB 1;  Length 25;
  Best Local Similarity   63.2%;  Pred. No. 2.9e+02;
  Matches   12;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTACAGGGAG 22
              || ||   || ||| | ||
Db         22 GCACTCGCTGCACACGTAG 4


RESULT 297
AX690107/c
LOCUS       AX690107                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 2839 from Patent EP1281758.
ACCESSION   AX690107
VERSION     AX690107.1  GI:29412965
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 2839 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES            Location/Qualifiers
     source         1. .25
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"

  Query Match            27.9%;  Score 7.8;  DB 1;  Length 25;
  Best Local Similarity   63.2%;  Pred. No. 2.9e+02;
  Matches   12;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTACAGGGAG 22
              || ||   || ||| | ||
Db         25 GCACTCGCTGCACACGTAG 7


RESULT 298
AX690108/c
LOCUS       AX690108                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 2840 from Patent EP1281758.
ACCESSION   AX690108
VERSION     AX690108.1  GI:29412966
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 2840 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES            Location/Qualifiers
     source         1. .25
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"

  Query Match            27.9%;  Score 7.8;  DB 1;  Length 25;
  Best Local Similarity   63.2%;  Pred. No. 2.9e+02;
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  Matches   12;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTACAGGGAG 22
              || ||   || ||| | ||
Db         24 GCACTCGCTGCACACGTAG 6


RESULT 299
AX690111/c
LOCUS       AX690111                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 2843 from Patent EP1281758.
ACCESSION   AX690111
VERSION     AX690111.1  GI:29412969
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 2843 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 25;
  Best Local Similarity   63.2%;  Pred. No. 2.9e+02;
  Matches   12;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTACAGGGAG 22
              || ||   || ||| | ||
Db         21 GCACTCGCTGCACACGTAG 3


RESULT 300
AX690112/c
LOCUS       AX690112                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 2844 from Patent EP1281758.
ACCESSION   AX690112
VERSION     AX690112.1  GI:29412970
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 2844 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.9%;  Score 7.8;  DB 1;  Length 25;
  Best Local Similarity   63.2%;  Pred. No. 2.9e+02;
  Matches   12;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTACAGGGAG 22
              || ||   || ||| | ||
Db         20 GCACTCGCTGCACACGTAG 2


RESULT 301
AX096928/c
LOCUS       AX096928                  10 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 2106 from Patent WO0118250.
ACCESSION   AX096928
VERSION     AX096928.1  GI:13513196
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 2106 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             27.1%;  Score 7.6;  DB 1;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 1.3e+02;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAG 22
              :|||||||
Db         10 MCAGGGAG 3


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Job time : 2 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 19, 2004, 15:00:27 ; Search time 1 Seconds
(without alignments)
0.417 Million cell updates/sec

Title: US-10-024-396-3-COPY
Perfect score: 28
Sequence: 1 cgggccctacgtgtacagggagtccagg 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 585 seqs, 7450 residues

Total number of hits satisfying chosen parameters: 1170

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 737 summaries

Database : rngdb:* N. Geneseq

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20	71.4	20	1	AAL62639	Human CD36 antigen
c	2	20	71.4	20	1	AAL62640	Human CD36 antigen
	3	18.6	66.4	25	1	ADB01855	Human MDZ3 scannin
	4	18.6	66.4	25	1	ADB01856	Human MDZ3 scannin
	5	18.2	65.0	25	1	ADB01854	Human MDZ3 scannin
	6	18.2	65.0	25	1	ADB01853	Human MDZ3 scannin
	7	17.8	63.6	25	1	ADB01851	Human MDZ3 scannin
	8	17.8	63.6	25	1	ADB01852	Human MDZ3 scannin
	9	17.6	62.9	25	1	ADB01857	Human MDZ3 scannin
	10	16.8	60.0	25	1	ADB01850	Human MDZ3 scannin
	11	16.6	59.3	25	1	ADB01858	Human MDZ3 scannin
	12	14.4	51.4	17	1	ADB00349	Human MDZ3 scannin
	13	14.4	51.4	17	1	ADB00350	Human MDZ3 scannin
c	14	14.2	50.7	19	1	AAT77699	Wheat microsatelli
	15	14.2	50.7	21	1	AAT17883	IL-11 receptor alp
	16	13.8	49.3	17	1	ADB00353	Human MDZ3 scannin
	17	13.8	49.3	17	1	ADB00352	Human MDZ3 scannin
	18	13.8	49.3	17	1	ADB00351	Human MDZ3 scannin
	19	13.8	49.3	17	1	ADB00354	Human MDZ3 scannin
	20	13.4	47.9	17	1	ADB00348	Human MDZ3 scannin
c	21	13.4	47.9	18	1	AAQ87648	Chick antisense ol
c	22	13.4	47.9	20	1	ABK37942	Forward RT-PCR pri
c	23	13.2	47.1	19	1	ABL43666	Human chromosome 1
c	24	13.2	47.1	20	1	ABI97518	Capture oligonucle
	25	12.8	45.7	17	1	ADB00355	Human MDZ3 scannin
	26	12.8	45.7	19	1	AAA11710	Human prostate-spe
	27	12.6	45.0	19	1	AAT30766	Rat acetyl coenzym
	28	12.4	44.3	17	1	ADB00347	Human MDZ3 scannin
	29	12.4	44.3	19	1	AAT96656	Mouse tub gene pri
	30	12.4	44.3	19	1	AAA94649	Mouse tub gene PCR
	31	12.2	43.6	17	1	ABL46308	Mouse scavenger re
	32	12.2	43.6	17	1	ADB00356	Human MDZ3 scannin
c	33	12.2	43.6	18	1	AAQ82129	Chromosome 11 (loc
	34	12.2	43.6	18	1	AAV30176	Protein kinase cat
	35	12	42.9	17	1	ADB00346	Human MDZ3 scannin
	36	12	42.9	17	1	ADB00345	Human MDZ3 scannin
	37	11.8	42.1	16	1	AAA51767	CYP3A5 gene 5' fla
c	38	11.4	40.7	15	1	AAF45954	IGFBP2 oligonucleo
c	39	11.4	40.7	15	1	AAF45953	IGFBP2 oligonucleo
c	40	11.4	40.7	15	1	AAF45955	IGFBP2 oligonucleo
	41	11.2	40.0	16	1	AAQ99935	Human MTS1 RT-PCR
	42	11.2	40.0	16	1	AAT00727	Multiple tumour su
	43	11.2	40.0	16	1	AAT69788	P16 promoter prime
	44	11.2	40.0	16	1	AAV53838	Nucleotide sequenc
	45	11.2	40.0	16	1	AAV11257	Human MTS1 and MTS
	46	11.2	40.0	16	1	AAV70602	PCR primer X2B for
	47	11.2	40.0	16	1	AAA95654	Human P16 promoter
	48	11.2	40.0	16	1	AAZ48793	PCR primer for hum
	49	11.2	40.0	16	1	AAZ39993	PCR primer for hum
	50	11.2	40.0	16	1	AAA39372	Human P16 PCR prim
	51	11.2	40.0	16	1	AAA11186	Human multiple tum
	52	11.2	40.0	16	1	AAF58190	Primer #13. Homo
	53	11.2	40.0	16	1	AAS02583	PCR primer X2B use
	54	11.2	40.0	16	1	AAD04711	Human MTS and MTS1
	55	11.2	40.0	16	1	AAC83090	Primer X2B used in
c	56	11.2	40.0	16	1	ADC98469	NOT304 polymorphis
	57	11.2	40.0	17	1	AAF07226	Hammerhead ribozym
	58	11.2	40.0	17	1	ABA80105	HBA2 mutation corr
c	59	11.2	40.0	17	1	ABA80104	HBA2 mutation corr
	60	11.2	40.0	17	1	ADB00357	Human MDZ3 scannin
	61	11.2	40.0	17	1	ABZ61654	Human H-Ras DNAzym
c	62	10.8	38.6	15	1	AAX31582	Tag sequence of a
	63	10.8	38.6	15	1	AAZ62510	Substrate for HH r
	64	10.8	38.6	15	1	AAH74110	Primer #7 used in
c	65	10.8	38.6	15	1	ABS97123	Human CYP4501A1 pr
c	66	10.8	38.6	15	1	ABX32536	Human pancreatic c
	67	10.8	38.6	15	1	ABX00361	Hepatitis C virus
c	68	10.4	37.1	12	1	ABI00908	Oligonucleotide pr
	69	10.4	37.1	13	1	ABC37718	Oligonucleotide SE
c	70	10.4	37.1	13	1	ABC37719	Oligonucleotide SE
c	71	10.4	37.1	15	1	AAF47954	IGFBP3 oligonucleo
c	72	10.4	37.1	15	1	AAF46048	IGFBP2 oligonucleo
c	73	10.4	37.1	15	1	AAF46045	IGFBP2 oligonucleo
c	74	10.4	37.1	15	1	AAF46046	IGFBP2 oligonucleo
c	75	10.4	37.1	15	1	AAF46047	IGFBP2 oligonucleo
c	76	10.4	37.1	15	1	AAF47955	IGFBP3 oligonucleo
c	77	10.4	37.1	15	1	AAF47956	IGFBP3 oligonucleo
c	78	10.4	37.1	15	1	AAF47953	IGFBP3 oligonucleo
c	79	10.4	37.1	15	1	AAF45952	IGFBP2 oligonucleo
c	80	10.4	37.1	15	1	AAF45956	IGFBP2 oligonucleo
	81	10.4	37.1	15	1	ABQ88645	Human CFL1 ASO pro
c	82	10.2	36.4	15	1	AAA52434	TdT-expressing Ram
c	83	10.2	36.4	15	1	AAF45958	IGFBP2 oligonucleo
c	84	10.2	36.4	15	1	AAF46044	IGFBP2 oligonucleo
c	85	10.2	36.4	15	1	AAF46043	IGFBP2 oligonucleo
c	86	10	35.7	10	1	AAV50300	Yeast tag for addi
c	87	10	35.7	10	1	AAF33845	Yeast NORF gene SA
c	88	10	35.7	10	1	AAF38150	Yeast NORF gene SA
c	89	10	35.7	10	1	AAF33846	Yeast NORF gene SA
c	90	10	35.7	10	1	AAF37110	Yeast NORF gene SA
c	91	10	35.7	10	1	AAF33517	Yeast NORF gene SA
c	92	10	35.7	10	1	AAF33847	Yeast NORF gene SA
c	93	10	35.7	10	1	AAF33850	Yeast NORF gene SA
	94	10	35.7	10	1	ABL39518	Human ETFB primer-
c	95	10	35.7	11	1	ABQ86347	Human skin stress/
c	96	10	35.7	11	1	ABV68461	Human skin EST 624
	97	10	35.7	15	1	AAT54219	Human IL-5 hammerh
	98	10	35.7	15	1	AAZ62686	Substrate for HH r
c	99	10	35.7	15	1	AAF45957	IGFBP2 oligonucleo
c	100	10	35.7	15	1	ABL52152	Human PER1 allele
	101	10	35.7	15	1	ABL39464	Human ETFB allele-
	102	10	35.7	15	1	ABX00537	Hepatitis C virus
	103	9.8	35.0	13	1	AAV11020	Human ribozyme tar
	104	9.8	35.0	13	1	AAV11070	Human ribozyme tar
c	105	9.8	35.0	13	1	ABF13206	Oligonucleotide SE
	106	9.8	35.0	13	1	ABH18793	Oligonucleotide SE

c 107	9.8	35.0	13	1	ABH18792	Oligonucleotide SE
c 108	9.8	35.0	13	1	ABF13210	Oligonucleotide SE
109	9.8	35.0	13	1	ABF18031	Oligonucleotide SE
110	9.8	35.0	13	1	ABF04489	Oligonucleotide SE
111	9.8	35.0	13	1	ABF13207	Oligonucleotide SE
c 112	9.8	35.0	13	1	ABF18028	Oligonucleotide SE
113	9.8	35.0	13	1	ABF18029	Oligonucleotide SE
c 114	9.8	35.0	13	1	ABH11997	Oligonucleotide SE
115	9.8	35.0	13	1	ABH11996	Oligonucleotide SE
c 116	9.8	35.0	13	1	ABF18030	Oligonucleotide SE
c 117	9.8	35.0	13	1	ABF04488	Oligonucleotide SE
118	9.8	35.0	13	1	ABF13211	Oligonucleotide SE
119	9.8	35.0	14	1	AAQ83327	jub-B antisense ol
120	9.8	35.0	14	1	AAA26121	Oestrogen receptor
c 121	9.8	35.0	14	1	ACA60796	DNA fragment conta
122	9.8	35.0	14	1	AAL60777	Human HNF-1 alpha
c 123	9.8	35.0	15	1	AAQ26688	PDGF-B primer 1.
c 124	9.8	35.0	15	1	AAQ49379	Human PDGF-B PCR p
125	9.8	35.0	15	1	AAX09580	Human biallelic po
126	9.8	35.0	15	1	AAZ62504	Substrate for HH r
c 127	9.8	35.0	15	1	AAZ90850	Human NR8 gene pro
c 128	9.8	35.0	15	1	AAZ90834	Human NR8 gene pro
c 129	9.8	35.0	15	1	AAZ90885	Human NR8 gene pro
c 130	9.8	35.0	15	1	AAZ90922	Human NR8 gene pro
131	9.8	35.0	15	1	AAC88512	CREB 230 coding se
132	9.8	35.0	15	1	AAH18956	UCP3 polymorphism
133	9.8	35.0	15	1	AAF45854	IGFBP2 oligonucleo
c 134	9.8	35.0	15	1	AAF46041	IGFBP2 oligonucleo
135	9.8	35.0	15	1	AAF45852	IGFBP2 oligonucleo
136	9.8	35.0	15	1	AAF45853	IGFBP2 oligonucleo
c 137	9.8	35.0	15	1	AAF46042	IGFBP2 oligonucleo
c 138	9.8	35.0	15	1	ABL52157	Human PER1 allele
c 139	9.8	35.0	15	1	ABL39485	Human ETFB allele-
c 140	9.8	35.0	15	1	ABA03963	Human STK11 gene p
141	9.8	35.0	15	1	AAD43376	Human CYP3A5 gene
c 142	9.8	35.0	15	1	ABK11468	ASO primer #4, use
143	9.8	35.0	15	1	ABX00355	Hepatitis C virus
c 144	9.4	33.6	11	1	ABV67167	Human skin EST 495
c 145	9.4	33.6	11	1	ABV67783	Human skin EST 556
c 146	9.4	33.6	11	1	ABV65206	Human skin EST 299
c 147	9.4	33.6	11	1	ABV67685	Human skin EST 547
148	9.4	33.6	12	1	ABI40444	Oligonucleotide pr
c 149	9.4	33.6	12	1	ABH89502	Oligonucleotide pr
c 150	9.4	33.6	12	1	ABI54047	Oligonucleotide pr
c 151	9.4	33.6	12	1	ABI23376	Oligonucleotide pr
c 152	9.4	33.6	12	1	ABI21821	Oligonucleotide pr
153	9.4	33.6	13	1	ABF19283	Oligonucleotide SE
154	9.4	33.6	13	1	ABC62107	Oligonucleotide SE
155	9.4	33.6	13	1	ABF44695	Oligonucleotide SE
156	9.4	33.6	13	1	ABC69525	Oligonucleotide SE
c 157	9.4	33.6	13	1	ABC54450	Oligonucleotide SE
c 158	9.4	33.6	13	1	ABF19282	Oligonucleotide SE
c 159	9.4	33.6	13	1	ABF44694	Oligonucleotide SE
c 160	9.4	33.6	13	1	ABH01278	Oligonucleotide SE
c 161	9.4	33.6	13	1	ABF63816	Oligonucleotide SE
c 162	9.4	33.6	13	1	ABC18273	Oligonucleotide SE
c 163	9.4	33.6	13	1	ABF25737	Oligonucleotide SE
164	9.4	33.6	13	1	ABF71706	Oligonucleotide SE
165	9.4	33.6	13	1	ABH47552	Oligonucleotide SE
166	9.4	33.6	13	1	ABC54451	Oligonucleotide SE
c 167	9.4	33.6	13	1	ABH42658	Oligonucleotide SE
168	9.4	33.6	13	1	ABH07266	Oligonucleotide SE
169	9.4	33.6	13	1	ABH42837	Oligonucleotide SE
c 170	9.4	33.6	13	1	ABC51399	Oligonucleotide SE
c 171	9.4	33.6	13	1	ABH47553	Oligonucleotide SE
172	9.4	33.6	13	1	ABF63817	Oligonucleotide SE
c 173	9.4	33.6	13	1	ABH42836	Oligonucleotide SE
174	9.4	33.6	13	1	ABH01279	Oligonucleotide SE
c 175	9.4	33.6	13	1	ABH07267	Oligonucleotide SE
176	9.4	33.6	13	1	ABH42659	Oligonucleotide SE
177	9.4	33.6	13	1	ABC51398	Oligonucleotide SE
178	9.4	33.6	13	1	ABC18272	Oligonucleotide SE
c 179	9.4	33.6	13	1	ABC62106	Oligonucleotide SE
c 180	9.4	33.6	13	1	ABC69524	Oligonucleotide SE
181	9.4	33.6	13	1	ABF25736	Oligonucleotide SE
c 182	9.4	33.6	13	1	ABF71707	Oligonucleotide SE
183	9.4	33.6	14	1	AAV92058	Human C-raf target
c 184	9.2	32.9	14	1	AAQ52942	Herpes simplex vir
c 185	9.2	32.9	14	1	AAQ83430	c-fos antisense ol
186	9	32.1	10	1	AAA98696	Nucleic acid combi
187	9	32.1	10	1	AAA56564	Human macrophage g
188	9	32.1	10	1	AAH63189	Human colon epithe
c 189	9	32.1	10	1	AAH20567	Human MTR1 intron1
190	9	32.1	10	1	AAF37219	Yeast NORF gene SA
191	9	32.1	10	1	AAF40677	Yeast NORF gene SA
c 192	9	32.1	10	1	ABL39519	Human ETFB primer-
c 193	9	32.1	11	1	ABV67716	Human skin EST 550
c 194	9	32.1	11	1	ABV65836	Human skin EST 362
c 195	9	32.1	12	1	AAT11911	Antisense DNA to i
196	9	32.1	12	1	ABH73584	Oligonucleotide pr
197	9	32.1	13	1	AAV11022	Human ribozyme tar
198	9	32.1	13	1	AAV11018	Human ribozyme tar
c 199	9	32.1	13	1	ABC24101	Oligonucleotide SE
200	9	32.1	13	1	ABC24100	Oligonucleotide SE
201	9	32.1	13	1	ABC90236	Oligonucleotide SE
c 202	9	32.1	13	1	ABC90237	Oligonucleotide SE
c 203	9	32.1	17	1	AAF07226	Hammerhead ribozym
c 204	8.8	31.4	12	1	AAZ41850	Organic material d
c 205	8.8	31.4	12	1	AAZ41634	Microbe detection
c 206	8.8	31.4	12	1	AAC97985	Primer used to ill
207	8.8	31.4	12	1	ABH71898	Oligonucleotide pr
208	8.8	31.4	12	1	ABI23374	Oligonucleotide pr
c 209	8.8	31.4	12	1	ABI26921	Oligonucleotide pr
c 210	8.8	31.4	12	1	ABI17179	Oligonucleotide pr
211	8.8	31.4	12	1	ABH71301	Oligonucleotide pr
c 212	8.8	31.4	12	1	ABH73583	Oligonucleotide pr
213	8.8	31.4	12	1	ABH75458	Oligonucleotide pr
c 214	8.8	31.4	12	1	ABI10854	Oligonucleotide pr
215	8.8	31.4	12	1	ABI37455	Oligonucleotide pr
216	8.8	31.4	12	1	ABI00095	Oligonucleotide pr
c 217	8.8	31.4	12	1	ABI68722	Oligonucleotide pr
c 218	8.8	31.4	12	1	ABI72643	Oligonucleotide pr
c 219	8.8	31.4	12	1	ABI59103	Oligonucleotide pr
220	8.8	31.4	12	1	ABI19821	Oligonucleotide pr
c 221	8.8	31.4	12	1	ABH70982	Oligonucleotide pr
222	8.8	31.4	12	1	ABI28323	Oligonucleotide pr
c 223	8.8	31.4	12	1	ABH73586	Oligonucleotide pr
c 224	8.8	31.4	12	1	ABH81956	Oligonucleotide pr
225	8.8	31.4	12	1	ABI18399	Oligonucleotide pr
226	8.8	31.4	12	1	ABI00093	Oligonucleotide pr
227	8.8	31.4	12	1	ABH84553	Oligonucleotide pr
228	8.8	31.4	12	1	ABI55944	Oligonucleotide pr
229	8.8	31.4	12	1	ABI01714	Oligonucleotide pr
230	8.8	31.4	12	1	ABH99794	Oligonucleotide pr
231	8.8	31.4	12	1	ABH72448	Oligonucleotide pr
232	8.8	31.4	12	1	ABH79191	Oligonucleotide pr
233	8.8	31.4	12	1	ABI78777	Oligonucleotide pr
c 234	8.8	31.4	12	1	ABH82234	Oligonucleotide pr
235	8.8	31.4	12	1	ADB81359	Bacteriophage C31-
236	8.8	31.4	13	1	AAV11023	Human ribozyme tar
237	8.8	31.4	13	1	AAV11115	Human ribozyme tar
c 238	8.8	31.4	13	1	AAV11113	Human ribozyme tar
239	8.8	31.4	13	1	AAV11114	Human ribozyme tar
c 240	8.8	31.4	13	1	ABC25956	Oligonucleotide SE
c 241	8.8	31.4	13	1	ABC37721	Oligonucleotide SE
c 242	8.8	31.4	13	1	ABF36729	Oligonucleotide SE
c 243	8.8	31.4	13	1	ABF77240	Oligonucleotide SE
244	8.8	31.4	13	1	ABH11994	Oligonucleotide SE
c 245	8.8	31.4	13	1	ABH11995	Oligonucleotide SE
246	8.8	31.4	13	1	ABC25957	Oligonucleotide SE
c 247	8.8	31.4	13	1	ABC05016	Oligonucleotide SE
248	8.8	31.4	13	1	ABC59500	Oligonucleotide SE
c 249	8.8	31.4	13	1	ABC37805	Oligonucleotide SE
c 250	8.8	31.4	13	1	ABC64857	Oligonucleotide SE
251	8.8	31.4	13	1	ABC64858	Oligonucleotide SE
252	8.8	31.4	13	1	ABF21570	Oligonucleotide SE

	253	8.8	31.4	13	1	ABF77241	Oligonucleotide SE
c	254	8.8	31.4	13	1	ABF60519	Oligonucleotide SE
c	255	8.8	31.4	13	1	ABF87825	Oligonucleotide SE
c	256	8.8	31.4	13	1	ABF89999	Oligonucleotide SE
c	257	8.8	31.4	13	1	ABF91303	Oligonucleotide SE
	258	8.8	31.4	13	1	ABC64856	Oligonucleotide SE
c	259	8.8	31.4	13	1	ABF74652	Oligonucleotide SE
	260	8.8	31.4	13	1	ABH30582	Oligonucleotide SE
c	261	8.8	31.4	13	1	ABH48420	Oligonucleotide SE
	262	8.8	31.4	13	1	ABH48421	Oligonucleotide SE
c	263	8.8	31.4	13	1	ABC49804	Oligonucleotide SE
	264	8.8	31.4	13	1	ABC49805	Oligonucleotide SE
c	265	8.8	31.4	13	1	ABH64062	Oligonucleotide SE
	266	8.8	31.4	13	1	ABC11970	Oligonucleotide SE
c	267	8.8	31.4	13	1	ABC37715	Oligonucleotide SE
c	268	8.8	31.4	13	1	ABC62971	Oligonucleotide SE
	269	8.8	31.4	13	1	ABF59322	Oligonucleotide SE
	270	8.8	31.4	13	1	ABF60516	Oligonucleotide SE
c	271	8.8	31.4	13	1	ABH37108	Oligonucleotide SE
	272	8.8	31.4	13	1	ABF87824	Oligonucleotide SE
c	273	8.8	31.4	13	1	ABC76137	Oligonucleotide SE
c	274	8.8	31.4	13	1	ABC56486	Oligonucleotide SE
	275	8.8	31.4	13	1	ABC60698	Oligonucleotide SE
c	276	8.8	31.4	13	1	ABC37725	Oligonucleotide SE
	277	8.8	31.4	13	1	ABC62970	Oligonucleotide SE
	278	8.8	31.4	13	1	ABF36730	Oligonucleotide SE
c	279	8.8	31.4	13	1	ABF36731	Oligonucleotide SE
c	280	8.8	31.4	13	1	ABF82918	Oligonucleotide SE
	281	8.8	31.4	13	1	ABC85926	Oligonucleotide SE
	282	8.8	31.4	13	1	ABC37714	Oligonucleotide SE
	283	8.8	31.4	13	1	ABC37724	Oligonucleotide SE
	284	8.8	31.4	13	1	ABF40375	Oligonucleotide SE
c	285	8.8	31.4	13	1	ABF97836	Oligonucleotide SE
	286	8.8	31.4	13	1	ABF87826	Oligonucleotide SE
	287	8.8	31.4	13	1	ABF91302	Oligonucleotide SE
c	288	8.8	31.4	13	1	ABC57873	Oligonucleotide SE
c	289	8.8	31.4	13	1	ABC62969	Oligonucleotide SE
	290	8.8	31.4	13	1	ABH35428	Oligonucleotide SE
	291	8.8	31.4	13	1	ABH43779	Oligonucleotide SE
c	292	8.8	31.4	13	1	ABC60701	Oligonucleotide SE
	293	8.8	31.4	13	1	ABC62968	Oligonucleotide SE
c	294	8.8	31.4	13	1	ABF21571	Oligonucleotide SE
	295	8.8	31.4	13	1	ABF36728	Oligonucleotide SE
	296	8.8	31.4	13	1	ABH13931	Oligonucleotide SE
	297	8.8	31.4	13	1	ABC57872	Oligonucleotide SE
c	298	8.8	31.4	13	1	ABC11971	Oligonucleotide SE
c	299	8.8	31.4	13	1	ABH13930	Oligonucleotide SE
c	300	8.8	31.4	13	1	ABH65565	Oligonucleotide SE
c	301	8.8	31.4	13	1	ABF20036	Oligonucleotide SE
	302	8.8	31.4	13	1	ABH30568	Oligonucleotide SE
c	303	8.8	31.4	13	1	ABF60517	Oligonucleotide SE
	304	8.8	31.4	13	1	ABH64063	Oligonucleotide SE
c	305	8.8	31.4	13	1	ABC50869	Oligonucleotide SE
c	306	8.8	31.4	13	1	ABC59501	Oligonucleotide SE
	307	8.8	31.4	13	1	ABF97837	Oligonucleotide SE
c	308	8.8	31.4	13	1	ABH35429	Oligonucleotide SE
c	309	8.8	31.4	13	1	ABF87829	Oligonucleotide SE
	310	8.8	31.4	13	1	ABC50868	Oligonucleotide SE
	311	8.8	31.4	13	1	ABF74653	Oligonucleotide SE
c	312	8.8	31.4	13	1	ABH30569	Oligonucleotide SE
	313	8.8	31.4	13	1	ABF89998	Oligonucleotide SE
	314	8.8	31.4	13	1	ABC43390	Oligonucleotide SE
c	315	8.8	31.4	13	1	ABC43391	Oligonucleotide SE
c	316	8.8	31.4	13	1	ABC60699	Oligonucleotide SE
	317	8.8	31.4	13	1	ABC37804	Oligonucleotide SE
c	318	8.8	31.4	13	1	ABF40374	Oligonucleotide SE
	319	8.8	31.4	13	1	ABH37109	Oligonucleotide SE
	320	8.8	31.4	13	1	ABC76136	Oligonucleotide SE
	321	8.8	31.4	13	1	ABC05017	Oligonucleotide SE
	322	8.8	31.4	13	1	ABC60700	Oligonucleotide SE
	323	8.8	31.4	13	1	ABF20037	Oligonucleotide SE
c	324	8.8	31.4	13	1	ABH30583	Oligonucleotide SE
	325	8.8	31.4	13	1	ABF60518	Oligonucleotide SE
c	326	8.8	31.4	13	1	ABH43778	Oligonucleotide SE
	327	8.8	31.4	13	1	ABH65564	Oligonucleotide SE
	328	8.8	31.4	13	1	ABC56487	Oligonucleotide SE
c	329	8.8	31.4	13	1	ABC85927	Oligonucleotide SE
	330	8.8	31.4	13	1	ABC37720	Oligonucleotide SE
c	331	8.8	31.4	13	1	ABC64859	Oligonucleotide SE
	332	8.8	31.4	13	1	ABF82919	Oligonucleotide SE
c	333	8.8	31.4	13	1	ABF59323	Oligonucleotide SE
c	334	8.8	31.4	13	1	ABF87827	Oligonucleotide SE
	335	8.8	31.4	13	1	ABF87828	Oligonucleotide SE
	336	8.8	31.4	13	1	ABZ72790	Rod opsin hammerhe
	337	8.8	31.4	13	1	ADD50029	Specific nucleic a
c	338	8.6	30.7	13	1	ABC35484	Oligonucleotide SE
	339	8.6	30.7	13	1	ABF27735	Oligonucleotide SE
c	340	8.6	30.7	13	1	ABC01632	Oligonucleotide SE
c	341	8.6	30.7	13	1	ABC09239	Oligonucleotide SE
	342	8.6	30.7	13	1	ABF95262	Oligonucleotide SE
c	343	8.6	30.7	13	1	ABF20736	Oligonucleotide SE
c	344	8.6	30.7	13	1	ABC61865	Oligonucleotide SE
c	345	8.6	30.7	13	1	ABF95263	Oligonucleotide SE
c	346	8.6	30.7	13	1	ABF84330	Oligonucleotide SE
	347	8.6	30.7	13	1	ABH01272	Oligonucleotide SE
	348	8.6	30.7	13	1	ABH64362	Oligonucleotide SE
c	349	8.6	30.7	13	1	ABH64363	Oligonucleotide SE
	350	8.6	30.7	13	1	ABC01633	Oligonucleotide SE
	351	8.6	30.7	13	1	ABC61864	Oligonucleotide SE
	352	8.6	30.7	13	1	ABF84331	Oligonucleotide SE
c	353	8.6	30.7	13	1	ABH01273	Oligonucleotide SE
	354	8.6	30.7	13	1	ABC09238	Oligonucleotide SE
	355	8.6	30.7	13	1	ABC35485	Oligonucleotide SE
c	356	8.6	30.7	13	1	ABF27734	Oligonucleotide SE
	357	8.6	30.7	13	1	ABF20737	Oligonucleotide SE
c	358	8.4	30.0	10	1	AAQ51822	mdr-1 mRNA ribozym
c	359	8.4	30.0	10	1	AAV48046	Human B7-2 targett
	360	8.4	30.0	10	1	AAZ84063	Metastatic breast
c	361	8.4	30.0	10	1	AAZ84365	Metastatic breast
	362	8.4	30.0	10	1	AAZ84677	Metastatic breast
c	363	8.4	30.0	10	1	AAZ81464	Metastatic breast
	364	8.4	30.0	10	1	AAZ83955	Metastatic breast
c	365	8.4	30.0	10	1	AAZ84972	Metastatic breast
c	366	8.4	30.0	10	1	AAZ85775	Metastatic breast
	367	8.4	30.0	10	1	AAZ82697	Metastatic breast
	368	8.4	30.0	10	1	AAZ79793	Human cystic kidne
c	369	8.4	30.0	10	1	AAF32888	Human B7-2 mRNA an
c	370	8.4	30.0	10	1	AAH20000	Mouse Treg immunor
c	371	8.4	30.0	10	1	AAH64417	Human ubiquitously
c	372	8.4	30.0	10	1	ABA06027	Human normal hepat
c	373	8.4	30.0	10	1	AAF40935	Yeast NORF gene SA
	374	8.4	30.0	10	1	AAF40704	Yeast NORF gene SA
c	375	8.4	30.0	10	1	AAF43233	Yeast NORF gene SA
	376	8.4	30.0	10	1	AAD25443	Human GNRH2 gene p
c	377	8.4	30.0	10	1	ABL52206	Human PER1 preferr
c	378	8.4	30.0	10	1	ABL52211	Human PER1 preferr
c	379	8.4	30.0	10	1	AAS98842	Colony stimulating
	380	8.4	30.0	10	1	ABK17003	Pyridoxal (Pyridox
c	381	8.4	30.0	10	1	AAD26864	Human GPR4 gene po
c	382	8.4	30.0	10	1	ABV84518	Human HCC underexp
c	383	8.4	30.0	10	1	ABV84755	Chronic hepatitis
c	384	8.4	30.0	10	1	ABV84794	Human apolipoprote
c	385	8.4	30.0	10	1	ABV84893	Human apolipoprote
	386	8.4	30.0	10	1	ABK81313	Human ADMR gene al
	387	8.4	30.0	10	1	AAD43418	Human CYP3A5 gene
	388	8.4	30.0	10	1	ABK64079	Human BF gene alle
	389	8.4	30.0	10	1	AAD25027	Human AANAT gene p
	390	8.4	30.0	10	1	AAD32316	Human neurotrophin
c	391	8.4	30.0	10	1	AAD47781	Human GNB3 gene po
	392	8.4	30.0	10	1	ACC78765	Normal estrogen re
	393	8.4	30.0	10	1	AAD53538	Human GNRH2 gene p
	394	8.4	30.0	10	1	AAD60113	Human androgen-reg
c	395	8.4	30.0	10	1	ADD71263	Mouse ET gene 5' s
c	396	8.4	30.0	10	1	ADE27823	Human B7-2 mRNA ta
c	397	8.4	30.0	11	1	AAV48047	Human B7-2 targett
c	398	8.4	30.0	11	1	AAZ18735	Murine C57BL/6 SAG

399	8.4	30.0	11	1	AAA35948	Human genomic DNA
400	8.4	30.0	11	1	AAC63231	Oligonucleotide #4
c 401	8.4	30.0	11	1	AAF32889	Human B7-2 mRNA an
402	8.4	30.0	11	1	AAF31235	Novel BAC vector c
403	8.4	30.0	11	1	AAS02836	Human pregnane X r
c 404	8.4	30.0	11	1	AAS02837	Human pregnane X r
c 405	8.4	30.0	11	1	ABQ86448	Human skin stress/
406	8.4	30.0	11	1	ABQ86579	Human skin stress/
407	8.4	30.0	11	1	ABQ86675	Human skin stress/
c 408	8.4	30.0	11	1	ABQ87015	Human skin stress/
409	8.4	30.0	11	1	ABQ86467	Human skin stress/
c 410	8.4	30.0	11	1	ABV68538	Human skin EST 632
c 411	8.4	30.0	11	1	ABV63286	Human skin EST 107
c 412	8.4	30.0	11	1	ABV71898	Human skin EST 968
413	8.4	30.0	11	1	ABV64207	Human skin EST 199
414	8.4	30.0	11	1	ABV70008	Human skin EST 779
415	8.4	30.0	11	1	ABV70593	Human skin EST 837
c 416	8.4	30.0	11	1	ABV62919	Human skin EST 705
417	8.4	30.0	11	1	ABV71628	Human skin EST 941
418	8.4	30.0	11	1	ABV64991	Human skin EST 277
c 419	8.4	30.0	11	1	ABV69231	Human skin EST 701
420	8.4	30.0	11	1	ABV63172	Human skin EST 958
421	8.4	30.0	11	1	ABV62587	Human skin EST 373
c 422	8.4	30.0	11	1	ABV62625	Human skin EST 411
c 423	8.4	30.0	11	1	ABV64477	Human skin EST 226
424	8.4	30.0	11	1	ABV66356	Human skin EST 414
425	8.4	30.0	11	1	ABV68439	Human skin EST 622
c 426	8.4	30.0	11	1	ABV70340	Human skin EST 812
c 427	8.4	30.0	11	1	ABV70707	Human skin EST 849
c 428	8.4	30.0	11	1	ABV70046	Human skin EST 783
429	8.4	30.0	11	1	ABK99385	Human CYP3A5 gene
c 430	8.4	30.0	11	1	ADE27824	Human B7-2 mRNA ta
431	8.4	30.0	12	1	AAQ52961	Herpes simplex vir
c 432	8.4	30.0	12	1	AAX79383	HLA-DR typing prob
c 433	8.4	30.0	12	1	AAT11933	Antisense DNA to i
c 434	8.4	30.0	12	1	AAV48048	Human B7-2 targett
c 435	8.4	30.0	12	1	AAV16579	Probe F67 used to
c 436	8.4	30.0	12	1	AAZ41746	Organic material d
c 437	8.4	30.0	12	1	AAZ41530	Microbe detection
438	8.4	30.0	12	1	AAA52398	TdT-expressing Ram
c 439	8.4	30.0	12	1	AAF32890	Human B7-2 mRNA an
c 440	8.4	30.0	12	1	AAC97881	Primer used to ill
c 441	8.4	30.0	12	1	ABH94723	Oligonucleotide pr
442	8.4	30.0	12	1	ABI06355	Oligonucleotide pr
c 443	8.4	30.0	12	1	ABI07028	Oligonucleotide pr
444	8.4	30.0	12	1	ABH73958	Oligonucleotide pr
445	8.4	30.0	12	1	ABI24391	Oligonucleotide pr
446	8.4	30.0	12	1	ABI63508	Oligonucleotide pr
447	8.4	30.0	12	1	ABI22910	Oligonucleotide pr
448	8.4	30.0	12	1	ABI25222	Oligonucleotide pr
449	8.4	30.0	12	1	ABH76574	Oligonucleotide pr
c 450	8.4	30.0	12	1	ABH87306	Oligonucleotide pr
c 451	8.4	30.0	12	1	ABH71336	Oligonucleotide pr
452	8.4	30.0	12	1	ABI35820	Oligonucleotide pr
453	8.4	30.0	12	1	ABI65800	Oligonucleotide pr
c 454	8.4	30.0	12	1	ABH85342	Oligonucleotide pr
455	8.4	30.0	12	1	ABH98134	Oligonucleotide pr
c 456	8.4	30.0	12	1	ABH79179	Oligonucleotide pr
c 457	8.4	30.0	12	1	ABI77362	Oligonucleotide pr
c 458	8.4	30.0	12	1	ABI65126	Oligonucleotide pr
459	8.4	30.0	12	1	ABI16276	Oligonucleotide pr
460	8.4	30.0	12	1	ABI22691	Oligonucleotide pr
c 461	8.4	30.0	12	1	ABI06949	Oligonucleotide pr
c 462	8.4	30.0	12	1	ABI25808	Oligonucleotide pr
463	8.4	30.0	12	1	ABI30071	Oligonucleotide pr
464	8.4	30.0	12	1	ABI10705	Oligonucleotide pr
465	8.4	30.0	12	1	ABI37238	Oligonucleotide pr
c 466	8.4	30.0	12	1	ABI51683	Oligonucleotide pr
c 467	8.4	30.0	12	1	ABH74522	Oligonucleotide pr
c 468	8.4	30.0	12	1	ABH85340	Oligonucleotide pr
c 469	8.4	30.0	12	1	AAF92639	HLA-DR typing prob
c 470	8.4	30.0	12	1	ABL59179	Oligonucleotide us
471	8.4	30.0	12	1	ADD68863	Human low homology
c 472	8.4	30.0	12	1	ADE27825	Human B7-2 mRNA ta
c 473	8.2	29.3	15	1	AAH74110	Primer #7 used in
c 474	8.2	29.3	17	1	ABZ61654	Human H-Ras DNAzym
475	8.2	29.3	20	1	AAL62639	Human CD36 antigen
476	8.2	29.3	20	1	AAL62640	Human CD36 antigen
c 477	8.2	29.3	21	1	AAT17883	IL-11 receptor alp
c 478	8	28.6	9	1	ABQ72155	Zinc finger protei
479	8	28.6	9	1	ABQ71897	Zinc finger protei
c 480	8	28.6	9	1	ABQ71800	Zinc finger protei
c 481	8	28.6	9	1	ABQ71802	Zinc finger protei
c 482	8	28.6	9	1	ABQ72156	Zinc finger protei
483	8	28.6	9	1	ADA64224	Zinc finger target
c 484	8	28.6	9	1	ADA64129	Zinc finger target
c 485	8	28.6	9	1	ADA64127	Zinc finger target
c 486	8	28.6	9	1	ADA64482	Zinc finger target
c 487	8	28.6	9	1	ADA64483	Zinc finger target
488	8	28.6	10	1	AAV50253	Yeast tag for addi
489	8	28.6	10	1	AAZ79208	Human dendritic ce
490	8	28.6	10	1	AAZ77621	Human dendritic ce
491	8	28.6	10	1	AAZ82875	Metastatic breast
492	8	28.6	10	1	AAZ83886	Metastatic breast
c 493	8	28.6	10	1	AAZ82564	Metastatic breast
c 494	8	28.6	10	1	AAZ82943	Metastatic breast
495	8	28.6	10	1	AAZ86367	Metastatic breast
c 496	8	28.6	10	1	AAZ79758	Human breast tumou
c 497	8	28.6	10	1	AAA74368	Mouse transcript t
498	8	28.6	10	1	AAF99919	Immunostimulatory
c 499	8	28.6	10	1	AAH64096	Human ubiquitously
c 500	8	28.6	10	1	AAH63834	Human ubiquitously
c 501	8	28.6	10	1	AAH63624	Human ubiquitously
c 502	8	28.6	10	1	AAH32824	LPS activated huma
503	8	28.6	10	1	AAH32796	LPS activated huma
504	8	28.6	10	1	ABA06035	Human normal hepat
c 505	8	28.6	10	1	AAF37857	Yeast NORF gene SA
506	8	28.6	10	1	AAF33470	Yeast NORF gene SA
507	8	28.6	10	1	AAF34993	Yeast NORF gene SA
508	8	28.6	10	1	AAF37881	Yeast NORF gene SA
c 509	8	28.6	10	1	AAF36719	Yeast NORF gene SA
c 510	8	28.6	10	1	AAF40202	Yeast NORF gene SA
511	8	28.6	10	1	AAF33645	Yeast NORF gene SA
c 512	8	28.6	10	1	AAF43177	Solute Carrier Fam
c 513	8	28.6	10	1	ABK95857	Human maturation/a
c 514	8	28.6	10	1	ABL42870	Human ALAS2 gene a
515	8	28.6	10	1	ABK37012	Human P450(cytochr
c 516	8	28.6	10	1	ABN80618	Human S-protein/so
517	8	28.6	10	1	ABV84803	Human S-protein/so
518	8	28.6	10	1	ABV84905	Transcript tag DNA
c 519	8	28.6	10	1	ABK23745	Human APOA4 ASO, p
520	8	28.6	10	1	AAS16755	Human apolipoprote
c 521	8	28.6	10	1	AAS16821	Interleukin 5 (IL5
522	8	28.6	10	1	AAS95473	Aldehyde dehydroge
523	8	28.6	10	1	AAS99418	Human CYP2E gene p
c 524	8	28.6	10	1	AAD51664	Nucleotide sequenc
c 525	8	28.6	11	1	AAA74982	Mutant tat HIV ret
526	8	28.6	11	1	AAZ39365	Nucleotide sequenc
c 527	8	28.6	11	1	AAA74965	Human skin stress/
528	8	28.6	11	1	ABQ87185	Human skin stress/
529	8	28.6	11	1	ABQ87673	Human skin stress/
530	8	28.6	11	1	ABQ86610	Human skin stress/
c 531	8	28.6	11	1	ABQ86755	Human skin stress/
c 532	8	28.6	11	1	ABQ86291	Human skin EST 630
c 533	8	28.6	11	1	ABV68516	Human skin EST 668
534	8	28.6	11	1	ABV68894	Human skin EST 801
c 535	8	28.6	11	1	ABV70231	Human skin EST 960
c 536	8	28.6	11	1	ABV71814	Human skin EST 101
537	8	28.6	11	1	ABV62315	Human skin EST 482
c 538	8	28.6	11	1	ABV67037	Human skin EST 860
539	8	28.6	11	1	ABV70819	Human skin EST 249
540	8	28.6	11	1	ABV64705	Human skin EST 596
c 541	8	28.6	11	1	ABV62810	Human skin EST 250
c 542	8	28.6	11	1	ABV64719	Human skin EST 289
543	8	28.6	11	1	ABV65110	Human skin EST 965
c 544	8	28.6	11	1	ABV71864	

	545	8	28.6	11	1	ABV65919	Human skin EST 370
	546	8	28.6	11	1	ABV63398	Human skin EST 118
c	547	8	28.6	11	1	ABV64393	Human skin EST 217
c	548	8	28.6	11	1	ABV64443	Human skin EST 222
	549	8	28.6	11	1	ABV72049	Human skin EST 983
	550	8	28.6	11	1	ABV69736	Human skin EST 752
	551	8	28.6	11	1	ABV66268	Human skin EST 405
c	552	8	28.6	11	1	ABV68998	Human skin EST 678
	553	8	28.6	11	1	ABL91942	Human Pan-Endothel
c	554	8	28.6	11	1	ABK68760	Oligonucleotide #6
	555	8	28.6	11	1	ABK68759	Oligonucleotide #5
c	556	8	28.6	11	1	ABL51577	Transferrin recept
	557	8	28.6	11	1	ABX71867	DNA tag used to id
	558	8	28.6	12	1	AAX79373	HLA-DR typing prob
c	559	8	28.6	12	1	AAT41818	HLA allele, HLA-DR
	560	8	28.6	12	1	AAV16569	Probe L74 used to
c	561	8	28.6	12	1	ABH93621	Oligonucleotide pr
c	562	8	28.6	12	1	ABI06748	Oligonucleotide pr
	563	8	28.6	12	1	ABH95544	Oligonucleotide pr
	564	8	28.6	12	1	ABI56358	Oligonucleotide pr
	565	8	28.6	12	1	ABH70251	Oligonucleotide pr
	566	8	28.6	12	1	ABH89284	Oligonucleotide pr
c	567	8	28.6	12	1	ABH92486	Oligonucleotide pr
	568	8	28.6	12	1	ABI13410	Oligonucleotide pr
	569	8	28.6	12	1	ABI62488	Oligonucleotide pr
	570	8	28.6	12	1	ABI13984	Oligonucleotide pr
c	571	8	28.6	12	1	ABH95542	Oligonucleotide pr
	572	8	28.6	12	1	ABH76707	Oligonucleotide pr
c	573	8	28.6	12	1	ABI76102	Oligonucleotide pr
	574	8	28.6	12	1	ABH81705	Oligonucleotide pr
c	575	8	28.6	12	1	ABH85829	Oligonucleotide pr
	576	8	28.6	12	1	ABH86354	Oligonucleotide pr
	577	8	28.6	12	1	ABI13988	Oligonucleotide pr
c	578	8	28.6	12	1	ABH97060	Oligonucleotide pr
	579	8	28.6	12	1	ABI16213	Oligonucleotide pr
	580	8	28.6	12	1	ABI56360	Oligonucleotide pr
c	581	8	28.6	12	1	ABI28945	Oligonucleotide pr
c	582	8	28.6	12	1	ABI10703	Oligonucleotide pr
c	583	8	28.6	12	1	ABI75403	Oligonucleotide pr
	584	8	28.6	12	1	ABI63259	Oligonucleotide pr
	585	8	28.6	12	1	ABH73580	Oligonucleotide pr
c	586	8	28.6	12	1	ABI56650	Oligonucleotide pr
c	587	8	28.6	12	1	ABI59399	Oligonucleotide pr
	588	8	28.6	12	1	AAF92629	HLA-DR typing prob
	589	8	28.6	12	1	AAF92695	HLA-DR allele grou
	590	8	28.6	12	1	ABL42258	Plant cis-regulato
	591	8	28.6	12	1	ABX10158	Human TIGR/Myocili
c	592	8	28.6	15	1	AAX09580	Human biallelic po
	593	7.8	27.9	11	1	ABV65206	Human skin EST 299
c	594	7.8	27.9	11	1	ABK99385	Human CYP3A5 gene
c	595	7.8	27.9	12	1	ABI23374	Oligonucleotide pr
c	596	7.8	27.9	12	1	ABI18399	Oligonucleotide pr
c	597	7.8	27.9	13	1	ABF18031	Oligonucleotide SE
	598	7.8	27.9	13	1	ABF18030	Oligonucleotide SE
c	599	7.8	27.9	13	1	ABF19283	Oligonucleotide SE
c	600	7.8	27.9	13	1	ABF44695	Oligonucleotide SE
	601	7.8	27.9	13	1	ABF19282	Oligonucleotide SE
	602	7.8	27.9	13	1	ABF44694	Oligonucleotide SE
c	603	7.8	27.9	13	1	ABF36730	Oligonucleotide SE
	604	7.8	27.9	13	1	ABF36731	Oligonucleotide SE
c	605	7.8	27.9	25	1	ADB01855	Human MDZ3 scannin
c	606	7.8	27.9	25	1	ADB01856	Human MDZ3 scannin
c	607	7.8	27.9	25	1	ADB01854	Human MDZ3 scannin
c	608	7.8	27.9	25	1	ADB01853	Human MDZ3 scannin
c	609	7.8	27.9	25	1	ADB01857	Human MDZ3 scannin
c	610	7.8	27.9	25	1	ADB01858	Human MDZ3 scannin
	611	7.6	27.1	15	1	AAF47954	IGFBP3 oligonucleo
	612	7.6	27.1	15	1	AAF47955	IGFBP3 oligonucleo
	613	7.6	27.1	15	1	AAF47956	IGFBP3 oligonucleo
c	614	7.6	27.1	17	1	ABA80105	HBA2 mutation corr
	615	7.6	27.1	17	1	ABA80104	HBA2 mutation corr
	616	7.4	26.4	10	1	ADD71263	Mouse ET gene 5' s
c	617	7.4	26.4	10	1	AAZ83886	Metastatic breast
	618	7.4	26.4	10	1	AAF37857	Yeast NORF gene SA
	619	7.4	26.4	12	1	ABH73586	Oligonucleotide pr
	620	7.4	26.4	18	1	AAQ87648	Chick antisense ol
	621	7.2	25.7	12	1	ABI23376	Oligonucleotide pr
c	622	7.2	25.7	12	1	ABH73584	Oligonucleotide pr
	623	7.2	25.7	12	1	AAZ41746	Organic material d
	624	7.2	25.7	12	1	AAZ41530	Microbe detection
	625	7.2	25.7	12	1	AAC97881	Primer used to ill
c	626	7.2	25.7	12	1	ABH73580	Oligonucleotide pr
c	627	7.2	25.7	13	1	ABH30582	Oligonucleotide SE
	628	7.2	25.7	13	1	ABC62971	Oligonucleotide SE
c	629	7.2	25.7	13	1	ABC62970	Oligonucleotide SE
	630	7.2	25.7	13	1	ABC62969	Oligonucleotide SE
c	631	7.2	25.7	13	1	ABC62968	Oligonucleotide SE
	632	7.2	25.7	13	1	ABH30583	Oligonucleotide SE
	633	7.2	25.7	15	1	AAA52434	TdT-expressing Ram
c	634	7.2	25.7	15	1	AAZ62686	Substrate for HH r
c	635	7.2	25.7	15	1	ABX00537	Hepatitis C virus
	636	7	25.0	10	1	AAF43233	Yeast NORF gene SA
	637	7	25.0	10	1	AAF36719	Yeast NORF gene SA
c	638	7	25.0	11	1	ABQ86579	Human skin stress/
c	639	7	25.0	11	1	ABV64991	Human skin EST 277
	640	7	25.0	15	1	AAZ90850	Human NR8 gene pro
	641	7	25.0	15	1	AAZ90834	Human NR8 gene pro
	642	7	25.0	15	1	AAZ90885	Human NR8 gene pro
	643	7	25.0	15	1	AAZ90922	Human NR8 gene pro
c	644	7	25.0	17	1	ABL46308	Mouse scavenger re
c	645	7	25.0	19	1	AAA11710	Human prostate-spe
	646	6.8	24.3	10	1	AAF38150	Yeast NORF gene SA
	647	6.8	24.3	10	1	AAF40202	Yeast NORF gene SA
	648	6.8	24.3	11	1	ABQ86347	Human skin stress/
	649	6.8	24.3	11	1	ABV68461	Human skin EST 624
c	650	6.8	24.3	12	1	ABH89284	Oligonucleotide pr
c	651	6.8	24.3	12	1	ABH76707	Oligonucleotide pr
	652	6.8	24.3	12	1	ABH85829	Oligonucleotide pr
	653	6.8	24.3	12	1	ABI10703	Oligonucleotide pr
c	654	6.8	24.3	13	1	AAV11115	Human ribozyme tar
	655	6.8	24.3	13	1	ABC09239	Oligonucleotide SE
c	656	6.8	24.3	13	1	ABC09238	Oligonucleotide SE
c	657	6.8	24.3	14	1	AAA26121	Oestrogen receptor
	658	6.8	24.3	14	1	AAQ83430	c-fos antisense ol
c	659	6.8	24.3	15	1	ABL39464	Human ETFB allele-
	660	6.8	24.3	15	1	ABA03963	Human STK11 gene p
c	661	6.8	24.3	16	1	AAA51767	CYP3A5 gene 5' fla
	662	6.8	24.3	19	1	AAT77699	Wheat microsatelli
c	663	6.8	24.3	25	1	ADB01852	Human MDZ3 scannin
c	664	6.6	23.6	13	1	AAV11022	Human ribozyme tar
	665	6.6	23.6	15	1	AAF47953	IGFBP3 oligonucleo
c	666	6.6	23.6	16	1	AAQ99935	Human MTS1 RT-PCR
c	667	6.6	23.6	16	1	AAT00727	Multiple tumour su
c	668	6.6	23.6	16	1	AAT69788	P16 promoter prime
c	669	6.6	23.6	16	1	AAV53838	Nucleotide sequenc
c	670	6.6	23.6	16	1	AAV11257	Human MTS1 and MTS
c	671	6.6	23.6	16	1	AAV70602	PCR primer X2B for
c	672	6.6	23.6	16	1	AAA95654	Human P16 promoter
c	673	6.6	23.6	16	1	AAZ48793	PCR primer for hum
c	674	6.6	23.6	16	1	AAZ39993	PCR primer for hum
c	675	6.6	23.6	16	1	AAA39372	Human P16 PCR prim
c	676	6.6	23.6	16	1	AAA11186	Human multiple tum
c	677	6.6	23.6	16	1	AAF58190	Primer #13. Homo
c	678	6.6	23.6	16	1	AAS02583	PCR primer X2B use
c	679	6.6	23.6	16	1	AAD04711	Human MTS and MTS1
c	680	6.6	23.6	16	1	AAC83090	Primer X2B used in
	681	6.4	22.9	10	1	AAZ79758	Human breast tumou
	682	6.4	22.9	11	1	ABV67783	Human skin EST 556
c	683	6.4	22.9	11	1	ABV70593	Human skin EST 837
c	684	6.4	22.9	11	1	ABV63172	Human skin EST 958
c	685	6.4	22.9	11	1	ABV70819	Human skin EST 860
c	686	6.4	22.9	11	1	ABV63398	Human skin EST 118
	687	6.4	22.9	12	1	ABH73583	Oligonucleotide pr
c	688	6.4	22.9	12	1	ABI10705	Oligonucleotide pr
c	689	6.4	22.9	12	1	ABI16213	Oligonucleotide pr
	690	6.4	22.9	13	1	ABC49804	Oligonucleotide SE

c 691	6.4	22.9	13	1	ABC49805	Oligonucleotide SE
692	6.4	22.9	13	1	ABC37725	Oligonucleotide SE
c 693	6.4	22.9	13	1	ABC37724	Oligonucleotide SE
c 694	6.4	22.9	17	1	ADB00353	Human MDZ3 scannin
c 695	6.4	22.9	17	1	ADB00354	Human MDZ3 scannin
c 696	6.4	22.9	17	1	ADB00356	Human MDZ3 scannin
c 697	6.4	22.9	17	1	ADB00357	Human MDZ3 scannin
c 698	6.4	22.9	25	1	ADB01851	Human MDZ3 scannin
c 699	6.4	22.9	25	1	ADB01850	Human MDZ3 scannin
700	6.2	22.1	12	1	ABI00908	Oligonucleotide pr
701	6.2	22.1	12	1	ABI54047	Oligonucleotide pr
702	6.2	22.1	12	1	ABI21821	Oligonucleotide pr
c 703	6.2	22.1	12	1	ABH71301	Oligonucleotide pr
c 704	6.2	22.1	12	1	ABI37455	Oligonucleotide pr
705	6.2	22.1	12	1	ABI72643	Oligonucleotide pr
c 706	6.2	22.1	12	1	ABH72448	Oligonucleotide pr
c 707	6.2	22.1	12	1	ABI22910	Oligonucleotide pr
708	6.2	22.1	13	1	ABF18028	Oligonucleotide SE
c 709	6.2	22.1	13	1	ABF18029	Oligonucleotide SE
c 710	6.2	22.1	13	1	ABC90236	Oligonucleotide SE
711	6.2	22.1	13	1	ABC90237	Oligonucleotide SE
712	6.2	22.1	13	1	ABF36729	Oligonucleotide SE
713	6.2	22.1	13	1	ABF60519	Oligonucleotide SE
c 714	6.2	22.1	13	1	ABF60516	Oligonucleotide SE
715	6.2	22.1	13	1	ABC56486	Oligonucleotide SE
716	6.2	22.1	13	1	ABF82918	Oligonucleotide SE
c 717	6.2	22.1	13	1	ABF36728	Oligonucleotide SE
718	6.2	22.1	13	1	ABF20036	Oligonucleotide SE
719	6.2	22.1	13	1	ABF60517	Oligonucleotide SE
c 720	6.2	22.1	13	1	ABF20037	Oligonucleotide SE
c 721	6.2	22.1	13	1	ABF60518	Oligonucleotide SE
c 722	6.2	22.1	13	1	ABC56487	Oligonucleotide SE
c 723	6.2	22.1	13	1	ABF82919	Oligonucleotide SE
724	6.2	22.1	15	1	AAF46048	IGFBP2 oligonucleo
725	6.2	22.1	15	1	AAF46045	IGFBP2 oligonucleo
726	6.2	22.1	15	1	AAF46046	IGFBP2 oligonucleo
727	6.2	22.1	15	1	AAF46047	IGFBP2 oligonucleo
c 728	6.2	22.1	15	1	AAT54219	Human IL-5 hammerh
c 729	6.2	22.1	17	1	ADB00349	Human MDZ3 scannin
c 730	6.2	22.1	17	1	ADB00350	Human MDZ3 scannin
c 731	6.2	22.1	17	1	ADB00352	Human MDZ3 scannin
c 732	6.2	22.1	17	1	ADB00351	Human MDZ3 scannin
c 733	6.2	22.1	17	1	ADB00348	Human MDZ3 scannin
734	6	21.4	9	1	ABQ72155	Zinc finger protei
735	6	21.4	9	1	ABQ72156	Zinc finger protei
736	6	21.4	9	1	ADA64482	Zinc finger target
737	6	21.4	9	1	ADA64483	Zinc finger target

ALIGNMENTS

```
RESULT 1
AAL62639/c
ID   AAL62639 standard; DNA; 20 BP.
XX
AC   AAL62639;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human CD36 antigen-like 1 (CD36L1) antisense oligo, ISIS 199306.
XX
KW   Human; CD36 antigen-like 1; CD36L1; scavenger receptor class B type 1;
KW   CLA-1; SRB1; SR-BI; cardiovascular; metabolic disorder; atherosclerosis;
KW   lipid metabolism; gene therapy; phosphorothioate backbone; antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003052062-A2.
XX
PD   26-JUN-2003.
XX
PF   09-DEC-2002; 2002WO-US039183.
XX
PR   18-DEC-2001; 2001US-00024396.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Dobie KW;
XX
DR   WPI; 2003-533006/50.
XX
PT   New compound, having a sequence targeted to a nucleic acid encoding
PT   CD36L1, useful for preparing a composition for treating
PT   hyperproliferative or autoimmune disorders.
XX
PS   Claim 3; Page 81; 122pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of class B scavenger receptor, CD36 antigen
CC   -like 1 (CD36L1). CD36L1 is also known as scavenger receptor class B type
CC   1 (SRB1), CLA-1 and mouse homologue, SR-BI. The antisense compound is
CC   useful for preparing a composition for treating metabolic or
CC   cardiovascular disorder, e.g. altered lipid metabolism or
CC   atherosclerosis. It is also used in gene therapy. The present sequence is
CC   an antisense oligonucleotide targetted to human CD36L1 DNA. This sequence
CC   is used to illustrate the method of the invention
XX
SQ   Sequence 20 BP; 3 A; 8 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match           71.4%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0.69;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCTACGTGTACAGGG 20
              ||||||||||||||||||||
Db         20 CGGGCCCTACGTGTACAGGG 1


RESULT 2
AAL62640/c
ID   AAL62640 standard; DNA; 20 BP.
XX
AC   AAL62640;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human CD36 antigen-like 1 (CD36L1) antisense oligo, ISIS 199307.
XX
KW   Human; CD36 antigen-like 1; CD36L1; scavenger receptor class B type 1;
KW   CLA-1; SRB1; SR-BI; cardiovascular; metabolic disorder; atherosclerosis;
KW   lipid metabolism; gene therapy; phosphorothioate backbone; antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
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FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003052062-A2.
XX
PD   26-JUN-2003.
XX
PF   09-DEC-2002; 2002WO-US039183.
XX
PR   18-DEC-2001; 2001US-00024396.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Dobie KW;
XX
DR   WPI; 2003-533006/50.
XX
PT   New compound, having a sequence targeted to a nucleic acid encoding
PT   CD36L1, useful for preparing a composition for treating
PT   hyperproliferative or autoimmune disorders.
XX
PS   Claim 3; Page 81; 122pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of class B scavenger receptor, CD36 antigen
CC   -like 1 (CD36L1). CD36L1 is also known as scavenger receptor class B type
CC   1 (SRB1), CLA-1 and mouse homologue, SR-BI. The antisense compound is
CC   useful for preparing a composition for treating metabolic or
CC   cardiovascular disorder, e.g. altered lipid metabolism or
CC   atherosclerosis. It is also used in gene therapy. The present sequence is
CC   an antisense oligonucleotide targetted to human CD36L1 DNA. This sequence
CC   is used to illustrate the method of the invention
XX
SQ   Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match            71.4%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0.69;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 ACGTGTACAGGGAGTCCAGG 28
              ||||||||||||||||||||
Db         20 ACGTGTACAGGGAGTCCAGG 1


RESULT 3
ADB01855
ID   ADB01855 standard; DNA; 25 BP.
XX
AC   ADB01855;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 2841.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 2841; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 3 A; 7 C; 10 G; 5 T; 0 U; 0 Other;

  Query Match            66.4%;  Score 18.6;  DB 1;  Length 25;
  Best Local Similarity  84.0%;  Pred. No. 2.3;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTACAGGGAGTCCAG 27
              |||||||||||| ||| |||| | |
Db          1 GGCCCTACGTGTGCAGCGAGTGCTG 25


RESULT 4
ADB01856
ID   ADB01856 standard; DNA; 25 BP.
XX
AC   ADB01856;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 2842.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
```

```
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 2842; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 3 A; 7 C; 10 G; 5 T; 0 U; 0 Other;

  Query Match             66.4%;  Score 18.6;  DB 1;  Length 25;
  Best Local Similarity   84.0%;  Pred. No. 2.3;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTACAGGGAGTCCAGG 28
              |||||||||||| ||| |||| | ||
Db          1 GCCCTACGTGTGCAGCGAGTGCTGG 25


RESULT 5
ADB01854
ID   ADB01854 standard; DNA; 25 BP.
XX
AC   ADB01854;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 2840.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 2840; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 4 A; 7 C; 9 G; 5 T; 0 U; 0 Other;

  Query Match             65.0%;  Score 18.2;  DB 1;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 2.9;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTACAGGGAGTCC 25
              |||||||||||| ||| |||| |
Db          2 GGCCCTACGTGTGCAGCGAGTGC 24


RESULT 6
ADB01853
ID   ADB01853 standard; DNA; 25 BP.
XX
AC   ADB01853;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 2839.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 2839; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
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CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 4 A; 7 C; 10 G; 4 T; 0 U; 0 Other;

  Query Match             65.0%;  Score 18.2;  DB 1;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 2.9;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTACAGGGAGTCC 25
              |||||||||||| ||| |||| |
Db          3 GGCCCTACGTGTGCAGCGAGTGC 25


RESULT 7
ADB01851
ID   ADB01851 standard; DNA; 25 BP.
XX
AC   ADB01851;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 2837.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 2837; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 6 A; 6 C; 9 G; 4 T; 0 U; 0 Other;

  Query Match             63.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 3.7;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTACAGGGAGT 23
              |||||||||||| ||| ||||
Db          5 GGCCCTACGTGTGCAGCGAGT 25


RESULT 8
ADB01852
ID   ADB01852 standard; DNA; 25 BP.
XX
AC   ADB01852;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 2838.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 2838; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 5 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

  Query Match             63.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 3.7;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTACAGGGAGT 23
```

```
                    ||||||||||||| ||| ||||
Db          4 GGCCCTACGTGTGCAGCGAGT 24


RESULT 9
ADB01857
ID   ADB01857 standard; DNA; 25 BP.
XX
AC   ADB01857;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 2843.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 2843; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 4 A; 7 C; 9 G; 5 T; 0 U; 0 Other;

  Query Match             62.9%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 4.1;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTACAGGGAGTCCAGG 28
              ||||||||||  ||| ||||  | ||
Db          1 CCCTACGTGTGCAGCGAGTGCTGG 24


RESULT 10
ADB01850
ID   ADB01850 standard; DNA; 25 BP.
XX
AC   ADB01850;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 2836.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 2836; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 7 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match             60.0%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 6.6;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTACAGGGAG 22
              ||||||||||||| ||| |||
Db          6 GGCCCTACGTGTGCAGCGAG 25


RESULT 11
ADB01858
ID   ADB01858 standard; DNA; 25 BP.
XX
AC   ADB01858;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 2844.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
```

KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 2844; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 5 A; 6 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 59.3%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 7.4;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 CCTACGTGTACAGGGAGTCCAGG 28
||||||||| ||| |||| | ||
Db 1 CCTACGTGTGCAGCGAGTGCTGG 23

RESULT 12
ADB00349
ID ADB00349 standard; DNA; 17 BP.
XX
AC ADB00349;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ3 scanning oligonucleotide SEQ ID 1335.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 1335; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 51.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 14;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGCCCTACGTGTACAG 18
||||||||||| |||
Db 2 GGCCCTACGTGTGCAG 17

RESULT 13
ADB00350
ID ADB00350 standard; DNA; 17 BP.
XX
AC ADB00350;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ3 scanning oligonucleotide SEQ ID 1336.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;

```
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 1336; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             51.4%;  Score 14.4;  DB 1;  Length 17;
  Best Local Similarity   93.8%;  Pred. No. 14;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTACAG 18
              ||||||||||||| |||
Db          1 GGCCCTACGTGTGCAG 16


RESULT 14
AAT77699/c
ID   AAT77699 standard; DNA; 19 BP.
XX
AC   AAT77699;
XX
DT   15-SEP-1997  (first entry)
XX
DE   Wheat microsatellite WMS261 left primer.
XX
KW   Microsatellite marker; hypervariable genomic fragment; Triticum aestivum;
KW   wheat; Triticeae; sequence tagged site; STS; primer; PCR; amplify;
KW   polymorphism; genetic analysis; hexaploid; tetraploid; mapping; ss.
XX
OS   Synthetic.
XX
PN   DE19525284-A1.
XX
PD   02-JAN-1997.
XX
PF   28-JUN-1995;   95DE-01025284.
XX
PR   28-JUN-1995;   95DE-01025284.
XX
PA   (PFLA-) INST PFLANZENGENETIK & KULTURPFLANZENFOR.
XX
PI   Roeder M,  Plaschke J,  Ganal M;
XX
DR   WPI; 1997-053731/06.
XX
PT   Primers for STS micro:satellite markers for wheat and related species -
PT   useful for genetic mapping, analysis and labelling etc. of wheat.
XX
PS   Claim 5; Page 8; 8pp; German.
XX
CC   Microsatellite markers based on hypervariable genomic fragments, from
CC   Triticum aestivum (wheat) or the tribe Triticeae, consist of a sequence
CC   tagged site (STS), defined by 2 specific primers (of mean size 17-23
CC   bases) that flank a microsatellite sequence at both ends, which can be
CC   amplified to polymorphisms (PCR products of different sizes). The
CC   microsatellites are n-fold tandem repeats (n = 10 or more) of di-, tri-
CC   or tetra-nucleotide sequences, combination microsatellite sequences or an
CC   imperfect sequence in which individual bases are mutated. The
CC   microsatellite markers can be used for genetic analysis of hexaploid and
CC   tetraploid forms of wheat and for genetic mapping or labelling of
CC   monogenic and polygenic properties, and for their selection; for
CC   analysing relationships and identifying varieties; and for evaluating
CC   varietal purity, hybrid identification and plant growth. The markers can
CC   differentiate between almost all European wheat lines and show a higher
CC   degree of DNA polymorphism than known probes for the wheat genome. They
CC   can be detected by PCR, so large numbers of samples can be analysed
CC   easily (e.g. several hundred per day). Microsatellite marker-related
CC   polymorphisms are stably inherited so can also serve as genetic markers.
CC   AAT77003-22 and AAT77535-716 are primer pairs that define the
CC   microsatellite markers. WMS261 has a CT type repeat
XX
SQ   Sequence 19 BP; 3 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             50.7%;  Score 14.2;  DB 1;  Length 19;
  Best Local Similarity   84.2%;  Pred. No. 19;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTACAGGGAG 22
              ||| || | ||||||||||
Db         19 GCCTTAGGCGTACAGGGAG 1


RESULT 15
AAT17883
ID   AAT17883 standard; DNA; 21 BP.
XX
AC   AAT17883;
XX
DT   21-MAY-1996  (first entry)
XX
DE   IL-11 receptor alpha chain probe 489.
XX
KW   Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
KW   therapy; diagnosis; probe; ss.
XX
OS   Synthetic.
XX
PN   WO9607737-A1.
XX
PD   14-MAR-1996.
XX
PF   05-SEP-1995;   95WO-AU000578.
XX
PR   05-SEP-1994;   94AU-00007901.
PR   05-SEP-1994;   94AU-00007902.
XX
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI   Hilton DJ;
XX
DR   WPI; 1996-171612/17.
XX
PT   Nucleic acid encoding haemopoietin receptor containing conserved amino
PT   acid motif esp. IL-11 receptor alpha chain - used for developing IL-11
PT   (ant)agonists.
XX
PS   Example 3; Page 21; 87pp; English.
XX
CC   Probe 489 (AAT17883) was used to detect interleukin-11 (IL-11) receptor
CC   alpha chain sequences following RT-PCR amplification of RNA from 15
CC   primary tissue samples and 17 cell lines. Nr1 mRNA (see AAT17868) was
CC   detected in 3T3-L1 cells, the stromal line BAd, the embryonic carcinoma
CC   cell line PC13 and the factor-dependent haemopoietin cell lines FDCP-1
CC   and D35 expressed Nr1 mRNA. Positive primary tissues included bone
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CC   marrow, spleen, thymus, liver, brain, heart kidney, muscle and salivary
CC   gland
XX
SQ   Sequence 21 BP; 3 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

  Query Match             50.7%;  Score 14.2;  DB 1;  Length 21;
  Best Local Similarity   84.2%;  Pred. No. 23;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCCAGG 28
              | |||||  ||||||||||
Db          3 CCTGTACTTGGAGTCCAGG 21


RESULT 16
ADB00353
ID   ADB00353 standard; DNA; 17 BP.
XX
AC   ADB00353;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 1339.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 1339; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             49.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 20;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACAGGGAG 22
              |||||||| ||| |||
Db          1 CCTACGTGTGCAGCGAG 17


RESULT 17
ADB00352
ID   ADB00352 standard; DNA; 17 BP.
XX
AC   ADB00352;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 1338.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 1338; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             49.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 20;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTACAGGGA 21
              |||||||||| ||| ||
Db          1 CCCTACGTGTGCAGCGA 17


RESULT 18
ADB00351
```

```
ID   ADB00351 standard; DNA; 17 BP.
XX
AC   ADB00351;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 1337.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 1337; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             49.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 20;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTACAGGG 20
              ||||||||||| ||| |
Db          1 GCCCTACGTGTGCAGCG 17


RESULT 19
ADB00354
ID   ADB00354 standard; DNA; 17 BP.
XX
AC   ADB00354;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 1340.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 1340; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             49.3%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 20;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGGGAGT 23
              |||||||| ||| ||||
Db          1 CTACGTGTGCAGCGAGT 17


RESULT 20
ADB00348
ID   ADB00348 standard; DNA; 17 BP.
XX
AC   ADB00348;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 1334.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
```

XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 1334; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

```
  Query Match             47.9%;  Score 13.4;  DB 1;  Length 17;
  Best Local Similarity   93.3%;  Pred. No. 26;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTACA 17
              ||||||||||||  ||
Db          3 GGCCCTACGTGTGCA 17
```

RESULT 21
AAQ87648/c
ID AAQ87648 standard; DNA; 18 BP.
XX
AC AAQ87648;
XX
DT 19-DEC-1995 (first entry)
XX
DE Chick antisense oligonucleotide to p75 NGFR gene.
XX
KW Oligonucleotide; antisense; down-regulation; expression; trauma;
KW nerve growth factor receptor; neurodegenerative disease; Alzheimer's;
KW Parkinson's; Hungtington's disease; multiple sclerosis;
KW vascular ischaemia; stroke; ss.
XX
OS Synthetic.
XX
PN WO9511253-A1.
XX
PD 27-APR-1995.
XX
PF 18-OCT-1994; 94WO-AU000631.
XX
PR 18-OCT-1993; 93AU-00001870.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Barrett GL;
XX
DR WPI; 1995-170186/22.
XX
PT Anti:sense oligo:nucleotide(s) to nerve growth factor receptor gene - of
PT p75 NGFR, down-regulate expression and enhance neurone survival; for
PT treating cerebal palsy, Alzheimer's disease, stroke, etc.
XX
PS Example 3; Page 35; 59pp; English.
XX
CC The sequence of an antisense oligonucleotide to the chick nerve growth
CC factor receptor (NGFR) gene which was used as a control for the survival
CC of mouse dorsal root ganglial (DRG) cells treated with oligonucleotides
CC AAQ87641-2. These oligonucleotides are antisense sequences directed at
CC down-regulating the expression of the gene encoding the mouse p75 NGFR
CC gene. The oligonucleotides can be used in methods to treat
CC neurodegenerative conditions associated with disease and/or trauma such
CC as Alzheimer's, Parkinson's or Hungtington's disease, multiple sclerosis,
CC vascular ischaemia associated with stroke, etc
XX
SQ Sequence 18 BP; 3 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

```
  Query Match             47.9%;  Score 13.4;  DB 1;  Length 18;
  Best Local Similarity   93.3%;  Pred. No. 28;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGTCCA 26
              ||||||| |||||||
Db         17 TGTACAGCGAGTCCA 3
```

RESULT 22
ABK37942/c
ID ABK37942 standard; DNA; 20 BP.
XX
AC ABK37942;
XX
DT 21-MAY-2002 (first entry)
XX
DE Forward RT-PCR primer for NOV3 #1.
XX
KW Human; NOVX; ss; cardiomyopathy; atherosclerosis; diabetes; PCR; primer;
KW cell signal processing disorder; metabolic disorder; obesity; infection;
KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;
KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;
KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;
KW psychosis; neurological disorder; anxiety; schizophrenia;
KW manic depression; dementia; dyskinesia; Huntington's disease;
KW Gilles de la Tourette's syndrome; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200210216-A2.
XX
PD 07-FEB-2002.
XX
PF 30-JUL-2001; 2001WO-US024225.
XX
PR 28-JUL-2000; 2000US-0221409P.
PR 04-AUG-2000; 2000US-0222840P.
PR 04-AUG-2000; 2000US-0223752P.
PR 04-AUG-2000; 2000US-0223762P.
PR 04-AUG-2000; 2000US-0223769P.
PR 04-AUG-2000; 2000US-0223770P.
PR 14-AUG-2000; 2000US-0225146P.
PR 15-AUG-2000; 2000US-0225392P.
PR 15-AUG-2000; 2000US-0225470P.
PR 16-AUG-2000; 2000US-0225697P.
PR 01-FEB-2001; 2001US-0263662P.
PR 05-APR-2001; 2001US-0281645P.

```
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Padigaru M,  Mezes P,  Mishra V,  Burgess C,  Casman S,  Grosse WM;
PI   Alsobrook JP,  Lepley DM,  Gerlach VL,  Macdougall JR,  Smithson G;
XX
DR   WPI; 2002-180074/23.
XX
PT   New isolated cytoplasmic, nuclear, membrane bound, or secreted
PT   polypeptide, useful for treating cardiomyopathy, atherosclerosis,
PT   infections, cancer, neurodegenerative, metabolic, hematopoietic and
PT   immune disorders.
XX
PS   Example 4; Page 156; 213pp; English.
XX
CC   The invention relates to an isolated cytoplasmic, nuclear, membrane
CC   bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
CC   form. Also included are the nucleic acids encoding the NOVX proteins, a
CC   vector comprising the nucleic acid, a cell comprising the vector, an anti
CC   -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
CC   antibody are useful for treating or preventing a NOVX-associated
CC   disorder, where the disorder is selected from cardiomyopathy,
CC   atherosclerosis, diabetes, a disorder related to cell signal processing
CC   and metabolic pathway modulation, metabolic disorders, obesity,
CC   infectious disease, anorexia, cancer-associated cachexia, cancer,
CC   neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
CC   immune disorders, haematopoietic disorders, and the various
CC   dyslipidaemias, metabolic disturbances associated with obesity, the
CC   metabolic syndrome X and wasting disorders associated with chronic
CC   diseases, bacterial, fungal, protozoal and viral infections, pain,
CC   bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's
CC   disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina
CC   pectoris, myocardial infarction, ulcer, allergy, benign prostatic
CC   hypertrophy, and psychotic and neurological disorders, including anxiety,
CC   schizophrenia, manic depression, delirium, dementia, and dyskinesias,
CC   such as Huntington's disease and Gilles de la Tourette's syndrome. The
CC   nucleic acid is useful in gene therapy. The present sequence is an RT-PCR
CC   (reverse transcriptase PCR) primer used to quantitate tissue specific
CC   expression of a NOVX transcript
XX
SQ   Sequence 20 BP; 2 A; 8 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             47.9%;  Score 13.4;  DB 1;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 33;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGTCCAGG 28
              || |||||||||||||
Db         17 TAGAGGGAGTCCAGG 3


RESULT 23
ABL43666/c
ID   ABL43666 standard; DNA; 19 BP.
XX
AC   ABL43666;
XX
DT   11-APR-2002  (first entry)
XX
DE   Human chromosome 1p36-35 PCR primer SEQ ID NO:710.
XX
KW   Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001321190-A.
XX
PD   20-NOV-2001.
XX
PF   12-MAR-2001; 2001JP-00068285.
XX
PR   10-MAR-2000; 2000JP-00066716.
XX
PA   (RIKA ) RIKAGAKU KENKYUSHO.
PA   (GENO-) GENOTEX YG.
XX
DR   WPI; 2002-144136/19.
XX
PT   Arraying genome clones.
XX
PS   Claim 4; Page 19; 528pp; Japanese.
XX
CC   The present invention describes a method of arraying genome clones. The
CC   method comprises: (a) clones of the genomic libraries contained in
CC   multiwell plates numbered for discrimination are mixed in each of the
CC   multiwell plates; (b) a primer designed based on the chromosome marker
CC   sequence is added to the mixture to carry out an amplification reaction;
CC   (c) a signal corresponding to the marker is detected from the resultant
CC   amplified product to specify the discrimination Nos. of the multiwell
CC   plates containing the clones having said marker sequence; (d) the order
CC   of the markers is changed so that the same discrimination Nos. succeed to
CC   the maximum in the specified discrimination Nos. to array the multiwell
CC   plates; (e) the clones in the multiwell plates of the specified
CC   discrimination Nos. are mixed respectively in each wells of longitudinal
CC   and lateral directions; (f) the mixed clones are cultured and the
CC   resultant cultures are amplified by using the above primer; (g) signals
CC   are detected from the amplified products; (h) the clones in the multiwell
CC   plates are specified from the detected result; and (i) the clones are
CC   reconstituted as the positions on the chromosome and arrayed. The
CC   microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC   PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC   represent PCR primers for human chromosome 21q22.1, which are
CC   specifically claimed for use in the present invention
XX
SQ   Sequence 19 BP; 4 A; 10 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             47.1%;  Score 13.2;  DB 1;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 35;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAGTCCAGG 28
              ||||| |||| | |||||
Db         19 GTGTAGAGGGTGGCCAGG 2


RESULT 24
ABI97518/c
ID   ABI97518 standard; DNA; 20 BP.
XX
AC   ABI97518;
XX
DT   16-FEB-2002  (first entry)
XX
DE   Capture oligonucleptide Zip ID#4605 oligo #9.
XX
KW   Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW   ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW   infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW   oncogene; tumour suppressor; human papillomavirus; forensic;
KW   environmental monitoring; food industry; feed industry; ss.
XX
OS   Synthetic.
XX
PN   WO200179548-A2.
XX
PD   25-OCT-2001.
XX
PF   04-APR-2001; 2001WO-US010958.
XX
PR   14-APR-2000; 2000US-0197271P.
XX
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Barany F,  Zirvi M,  Gerry NP,  Favis R,  Kliman R;
XX
```

```
DR   WPI; 2002-034366/04.
XX
PT   Designing capture oligonucleotide probes for use on a support to which
PT   complementary oligonucleotides hybridize with little mismatch.
XX
PS   Example 5; Fig 29; 300pp; English.
XX
CC   The present invention describes a method (M1) for designing capture
CC   oligonucleotide probes (I) for use on a support to which complementary
CC   oligonucleotide probes (II) will hybridise with little mismatch, where
CC   (I) have melting temperatures within a narrow range. The method is useful
CC   for detecting infectious diseases caused by bacterial infectious agents
CC   e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC   infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC   Aspergillus fumigautus, viruses e.g. T-cell lymphocytotrophis cirus,
CC   Epstein-Barr virus and polio virus, and parasitic infectious agents
CC   selected from Onchoverva volvulus, Entamoeba histolytica and Dracunculus
CC   medinesis. The method is also useful for detecting genetic diseases such
CC   as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC   Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC   involved in DNA amplification, replication, recombination or repair, the
CC   cancer is specifically associated with a gene selected from BRCA1 gene,
CC   p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC   method is also used for environmental monitoring, forensics and the food
CC   and feed industry, detecting comprises scanning (using e.g. a scanning
CC   electron microscope and infrared microscope) the support at the
CC   particular sites and identifying if ligation of the oligonucleotide probe
CC   sets occurred and correlating (using a computer) identified ligation to a
CC   presence or absence of the target nucleotide sequences. ABI82074 to
CC   ABI97546 represent oligonucleotide sequences used in the exemplification
CC   of the present invention
XX
SQ   Sequence 20 BP; 5 A; 9 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             47.1%;  Score 13.2;  DB 1;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 38;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCCAG 27
              |||||  |||||||||| |
Db         20 CGTGTGTAGGGAGTCCGG 3


RESULT 25
ADB00355
ID   ADB00355 standard; DNA; 17 BP.
XX
AC   ADB00355;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 1341.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 1341; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 3 A; 3 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             45.7%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 36;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGGGAGT 23
              ||||||| ||| ||||
Db          1 TACGTGTGCAGCGAGT 16


RESULT 26
AAA11710
ID   AAA11710 standard; DNA; 19 BP.
XX
AC   AAA11710;
XX
DT   14-JUL-2000  (first entry)
XX
DE   Human prostate-specific antigen PCR primer #4.
XX
KW   Prostate-specific antigen; PSA; detection; prostate cancer; PCR primer;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   JP2000069969-A.
XX
PD   07-MAR-2000.
XX
PF   28-AUG-1998;   98JP-00243419.
XX
PR   28-AUG-1998;   98JP-00243419.
XX
PA   (HITB ) HITACHI CHEM CO LTD.
PA   (NIID-) NIPPON IDENSHI KENKYUSHO KK.
XX
DR   WPI; 2000-264446/23.
XX
PT   A primer DNA and detection of an mRNA encoding a prostate-specific
PT   antigen by using it.
XX
PS   Claim 2; Page 9; 10pp; Japanese.
XX
CC   This invention describes novel primers used in a method of detecting an
CC   mRNA encoding prostate-specific antigen (PSA) in which cDNA synthesis is
CC   carried out by using an mRNA encoding PSA contained in a sample as the
CC   first template and then carrying out PCR using one of four described
CC   primers to generate a second template. A further a PCR is carried out to
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CC   generate a third template. The primer DNA is used for the specific
CC   detection of prostate cancer. The method is sensitive and specific.
CC   AAA11707-A11710 represent the PCR primers described in the method of the
CC   invention
XX
SQ   Sequence 19 BP; 4 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             45.7%;  Score 12.8;  DB 1;  Length 19;
  Best Local Similarity   87.5%;  Pred. No. 44;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACAGGGA 21
              |||  ||||||||||
Db          4 CCTTGGTGTACAGGGA 19


RESULT 27
AAT30766
ID   AAT30766 standard; DNA; 19 BP.
XX
AC   AAT30766;
XX
DT   10-FEB-1997  (first entry)
XX
DE   Rat acetyl coenzyme A carboxylase gene PCR primer 3'.
XX
KW   Acetyl coenzyme A carboxylase; ACoACase; Rattus; murine; ACCase;
KW   fatty acid biosynthesis; EC 6.4.1.2; polymerase chain reaction;
KW   complementation; ss.
XX
OS   Synthetic.
XX
PN   FR2727129-A1.
XX
PD   24-MAY-1996.
XX
PF   21-NOV-1994;   94FR-00014187.
XX
PR   21-NOV-1994;   94FR-00014187.
XX
PA   (RHON ) RHONE POULENC AGROCHIMIE.
XX
PI   Lebrun M,  Grosjean CMC,  Hollomon DW;
XX
DR   WPI; 1996-270416/28.
XX
PT   Microorganism with specific biochemical activity deleted by mutation -
PT   and complemented, used in system to identify cpds with plant protecting
PT   activity, also new gene for acetyl coenzyme A carboxylase.
XX
PS   Example 1; Page 6; 26pp; French.
XX
CC   The complete cDNA sequence coding for acetyl coenzyme A carboxylase
CC   (ACoACase, EC.6.4.1.2) from the rat was amplified in three parts using
CC   three separate pairs of PCR primers. The individual fragments were then
CC   ligated together to form the full-length cDNA. The present sequence is
CC   that of primer 3' which was used with primer 3 (see AAT30765). The rat
CC   ACoACase cDNA was shown to complement haploid yeast disrupted in the acc1
CC   gene (i.e. the yeast gene coding for ACoACase). Microorganisms which are
CC   mutated so that they lack a specific biochemical activity (esp. ACoACase
CC   activity) that can be complemented by a second microorganism are used in
CC   a novel screening system
XX
SQ   Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 12.6;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 49;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGGGAGTCC 25
              ||||||   |  ||||||||
Db          1 CTACGTAGAAGGGGAGTCC 19


RESULT 28
ADB00347
ID   ADB00347 standard; DNA; 17 BP.
XX
AC   ADB00347;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 1333.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 1333; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             44.3%;  Score 12.4;  DB 1;  Length 17;
  Best Local Similarity   92.9%;  Pred. No. 46;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTAC 16
              |||||||||||| |
Db          4 GGCCCTACGTGTGC 17


RESULT 29
AAT96656
ID   AAT96656 standard; cDNA; 19 BP.
XX
AC   AAT96656;
XX
DT   25-MAR-2003  (revised)
```

```
DT   27-APR-1998  (first entry)
XX
DE   Mouse tub gene primer C13R3.
XX
KW   TULP; tub gene; mouse; sensory neuron; neurosensory defect;
KW   cochlear degeneration; hearing loss; deafness; retinal dystrophy;
KW   retinitis pigmentosa; combined rod cone dystrophy; obesity; animal model;
KW   transgenic animal; therapy; diagnosis; PCR; primer; ss.
XX
OS   Synthetic.
OS   Mus musculus.
XX
PN   WO9738004-A1.
XX
PD   16-OCT-1997.
XX
PF   10-APR-1997;   97WO-US005903.
XX
PR   10-APR-1996;   96US-00630592.
PR   22-AUG-1996;   96US-00701380.
PR   04-SEP-1996;   96US-00706292.
PR   17-SEP-1996;   96US-00714991.
XX
PA   (SEQU-) SEQUANA THERAPEUTICS INC.
PA   (JACK-) JACKSON LAB.
XX
PI   Nishina P,  Nobentrauth K,  Naggert J,  North M;
XX
DR   WPI; 1997-512642/47.
XX
PT   Mammalian TULP protein - used for detecting pre-disposition to neuro-
PT   sensory defects.
XX
PS   Disclosure; Page 28; 89pp; English.
XX
CC   Primer C13R3 (AAT96656) and primer C13F3 (AAT96655) were used to obtain a
CC   mouse tub gene intron-specific probe DNA fragment for northern blots by
CC   amplifying mouse genomic DNA. Tub mutation is associated with adult onset
CC   obesity. Mouse Form I (see AAT96636) and Form II (see AAT96637) tub cDNAs
CC   have been isolated. Tub is a member of the mammalian TULP gene family
CC   associated with various defects in sensory neurons such as cochlear
CC   defects, retinitis pigmentosa and combined rod-cone dystrophy. (Updated
CC   on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 19 BP; 6 A; 3 C; 9 G; 1 T; 0 U; 0 Other;

  Query Match             44.3%;  Score 12.4;  DB 1;  Length 19;
  Best Local Similarity   92.9%;  Pred. No. 55;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAGTCCAGG 28
              ||||||| |||||
Db          6 ACAGGGAGACCAGG 19


RESULT 30
AAA94649
ID   AAA94649 standard; DNA; 19 BP.
XX
AC   AAA94649;
XX
DT   15-JAN-2001  (first entry)
XX
DE   Mouse tub gene PCR primer C13R3.
XX
KW   Mouse; TULP; neurosensory defect; retina; retinal dystrophy; PCR primer;
KW   TUB; ss.
XX
OS   Mus sp.
XX
PN   US6114502-A.
XX
PD   05-SEP-2000.
XX
PF   27-FEB-1998;   98US-00032365.
XX
PR   10-APR-1996;   96US-00630592.
PR   22-AUG-1996;   96US-00701380.
PR   04-SEP-1996;   96US-00706292.
PR   17-SEP-1996;   96US-00714991.
PR   30-APR-1997;   97US-00850218.
PR   01-AUG-1997;   97US-00904699.
PR   17-SEP-1997;   97US-00932306.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   North M,  Nishina P,  Noben-Trauth K,  Naggert J;
XX
DR   WPI; 2000-586483/55.
XX
PT   Mammalian proteins expressed in retina and brain, useful for producing
PT   antibodies and for diagnosing neurosensory defects including cochlear
PT   degeneration, peripheral retinal degeneration and cone-rod retinal
PT   dystrophy.
XX
PS   Disclosure; Col 21; 61pp; English.
XX
CC   The present invention relates to human and murine cDNAs from a
CC   neurosensory defect associated gene family. The novel cDNAs are mouse tub
CC   form I (see AAA94629), mouse tub form II (see AAA94630), human TUB form 6
CC   (see AAA94632), human TUB form 1 (see AAA94633), human TULP1 (see
CC   AAA94635), human TULP2 (see AAA94636), human TULP3 (see AAA94637) and
CC   mouse TULP4 (see AAA94638). The novel coding sequences are useful as
CC   immunogens to raise antibodies that specifically identify TUB/TULP
CC   expressing cells and in drug screening assays directed at neurosensory
CC   defects. The novel proteins encoded by the present sequence can be used
CC   for the treatment of neurosensory degenerative conditions e.g. retinal
CC   dystrophies. The present sequence is a PCR primer used to isolate the
CC   novel genes of the present invention
XX
SQ   Sequence 19 BP; 6 A; 3 C; 9 G; 1 T; 0 U; 0 Other;

  Query Match             44.3%;  Score 12.4;  DB 1;  Length 19;
  Best Local Similarity   92.9%;  Pred. No. 55;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAGTCCAGG 28
              ||||||| |||||
Db          6 ACAGGGAGACCAGG 19


RESULT 31
ABL46308
ID   ABL46308 standard; DNA; 17 BP.
XX
AC   ABL46308;
XX
DT   26-APR-2002  (first entry)
XX
DE   Mouse scavenger receptor class B type 1 oligonucleotide SEQ ID NO:275.
XX
KW   Nucleic acid accessible hybridisation site; detection; hybridisation;
KW   characterisation; identification; nucleic acid structure; diagnosis;
KW   PCR primer; probe; ss.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   WO200198537-A2.
XX
PD   27-DEC-2001.
XX
PF   15-JUN-2001; 2001WO-US019401.
XX
PR   17-JUN-2000; 2000US-0212308P.
PR   15-JUN-2001; 2001US-00212308.
```

```
XX
PA   (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI   Lyamichev V,  Allawi H,  Dong F,  Neri BP,  Vener IT;
XX
DR   WPI; 2002-049698/06.
XX
PT   Identifying oligonucleotides hybridizing to nucleic acids containing
PT   secondary structure, useful in clinical diagnosis, comprises identifying
PT   primers that interact with the target to form an extension product under
PT   amplification conditions.
XX
PS   Claim 48; Fig 79A; 409pp; English.
XX
CC   The present invention describes a method for identifying oligonucleotides
CC   with desired hybridisation properties to nucleic acid targets containing
CC   secondary structure. The method comprises amplifying a target nucleic
CC   acid having at least one accessible and one inaccessible site. Primers
CC   that form an extension product are identified as the oligonucleotides
CC   which can interact with the folded target nucleic acid. Oligonucleotides
CC   from the present invention can be used in novel detection methods for
CC   clinical diagnostic purposes, including the detection and identification
CC   of pathogenic organisms (e.g. HIV). The method allows the ability to
CC   rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
CC   sequences used in the exemplification of the present invention
XX
SQ   Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             43.6%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 51;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 GGGCCCTACGTGTACAG 18
              || ||||| || |||||
Db          1 GGACCCTATGTCTACAG 17


RESULT 32
ADB00356
ID   ADB00356 standard; DNA; 17 BP.
XX
AC   ADB00356;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 1342.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 1342; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             43.6%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 51;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          9 ACGTGTACAGGGAGTCC 25
              |||||| ||| |||| |
Db          1 ACGTGTGCAGCGAGTGC 17


RESULT 33
AAQ82129/c
ID   AAQ82129 standard; DNA; 18 BP.
XX
AC   AAQ82129;
XX
DT   25-MAR-2003  (revised)
DT   01-SEP-1995  (first entry)
XX
DE   Chromosome 11 (locus D11S1052) STS primer cSRL-2e7-tA.
XX
KW   sequence sampled mapping; genomic analysis; complex genome mapping;
KW   cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
XX
OS   Synthetic.
XX
PN   WO9429486-A1.
XX
PD   22-DEC-1994.
XX
PF   15-JUN-1994;   94WO-US006810.
XX
PR   15-JUN-1993;   93US-00078471.
PR   07-SEP-1993;   93US-00117952.
XX
PA   (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI   Evans GA,  Smith MW;
XX
DR   WPI; 1995-036508/05.
XX
PT   Sequencing complex genomes, present as fragments in a cosmid library - by
PT   sequencing end-specific nucleotides of each clone then correlating with
PT   spatial relationship of cosmid, esp. for mammalian chromosomes.
XX
PS   Example 4; Page 67; 128pp; English.
XX
CC   Sequences were determined from the ends of chromosome 11-specific cosmids
CC   by automated sequencing without intermediate subcloning. A sample of 371
CC   DNA sequence fragments were determined and of these, 277 were suitable
CC   for STS primer prediction by computer analysis (using the "Primer"
CC   program available from E.Lander, MIT). The STSs and cosmids were mapped
CC   by in situ hybridisation, somatic cell hybrid analysis or both. Using
CC   this method, 370 STSs specific for human chromosome 11 were generated and
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CC   most of them were regionally mapped. This procedure illustrates a novel
CC   method for sequencing complex genomes, designated "sequence sampled
CC   mapping". The sequence sampled mapping method is useful for the
CC   completion of high density sequence-based maps, and ultimately, for the
CC   complete sequencing of genomic DNA directly from cosmid clones. See
CC   AAQ82001-Q82706 for STS primers. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 18 BP; 3 A; 9 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             43.6%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 56;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAGTCCAG 27
              ||| | |||||||||| |
Db         18 GTGGAAAGGGAGTCCGG 2


RESULT 34
AAV30176
ID   AAV30176 standard; DNA; 18 BP.
XX
AC   AAV30176;
XX
DT   14-SEP-1998  (first entry)
XX
DE   Protein kinase catalytic subunit PCR primer 286.
XX
KW   Severe combined immunodeficiency disease; SCID; horse; diagnosis;
KW   DNA-dependent protein kinase; PCR; primer; ds.
XX
OS   Synthetic.
OS   Equus caballus.
XX
PN   WO9821367-A1.
XX
PD   22-MAY-1998.
XX
PF   14-NOV-1997;   97WO-US021066.
XX
PR   15-NOV-1996;   96US-0031261P.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Meeks K;
XX
DR   WPI; 1998-297967/26.
XX
PT   DNA-dependent protein kinase catalytic subunit - useful for determining
PT   equine severe combined immunodeficiency alleles.
XX
PS   Example 3; Page 19; 98pp; English.
XX
CC   Primer 286 was used in an RT-PCR strategy to clone and sequence equine
CC   DNA-dependent protein kinase catalytic subunit transcripts. Primer 286,
CC   and other primers used in the RT-PCR (see also AAV30171-93), are based on
CC   a published human DNA-dependent protein kinase catalytic subunit
CC   sequence. cDNA template was derived from 2 fibroblast cell lines, 0176
CC   (from a normal, non-Arabian horse) and 1821 (from a SCID foal). Sequence
CC   analysis showed that in SCID horses, a 5 bp deletion is present
CC   corresponding to nucleotide 9454 of the 12,381 nucleotide coding sequence
CC   of the human transcript. This results in premature termination of the
CC   catalytic subunit at amino acid 3160 (see AAW56642) of the polypeptide.
CC   Primers 405 and 392 (see AAV30192-93) can be used to screen for the
CC   mutant SCID allele. Methods are provided for identifying carriers of the
CC   mutation and for differentiating SCID homozygotes, heterozygotes and
CC   normal horses
XX
SQ   Sequence 18 BP; 5 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             43.6%;  Score 12.2;  DB 1;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 56;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGTCCAGG 28
              | |||||||| | ||||
Db          1 TCTACAGGGAATTCAGG 17


RESULT 35
ADB00346
ID   ADB00346 standard; DNA; 17 BP.
XX
AC   ADB00346;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 1332.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 1332; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 4 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             42.9%;  Score 12;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGT 14
              ||||||||||||
Db          5 GGCCCTACGTGT 16


RESULT 36
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```
ADB00345
ID   ADB00345 standard; DNA; 17 BP.
XX
AC   ADB00345;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 1331.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 1331; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             42.9%;  Score 12;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGT 14
              ||||||||||||
Db          6 GGCCCTACGTGT 17


RESULT 37
AAA51767
ID   AAA51767 standard; DNA; 16 BP.
XX
AC   AAA51767;
XX
DT   31-OCT-2000  (first entry)
XX
DE   CYP3A5 gene 5' flanking region forward sequencing primer 3A5p01.
XX
KW   CYP3A5; Cytochrome P450; transcription regulatory region; polymorphism;
KW   Activator protein-3 motif; AP-3; basic transcription element;
KW   drug metabolism; phenotype; sequencing primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200039332-A1.
XX
PD   06-JUL-2000.
XX
PF   22-DEC-1999;   99WO-GB004380.
XX
PR   23-DEC-1998;   98GB-00028619.
XX
PA   (JANC ) JANSSEN PHARM NV.
XX
PI   Paulussen ADC,  Armstrong M;
XX
DR   WPI; 2000-452418/39.
XX
PT   Identifying subjects with a high drug metabolizing phenotype associated
PT   with cytochrome CYP3A5 expression for establishing whether a drug will be
PT   metabolized by the subject.
XX
PS   Disclosure; Page 39; 68pp; English.
XX
CC   Cytochrome P450 subfamily CYP3A5 transcription regulatory regions can be
CC   screened for the presence/absence of a polymorphic variant, preferably at
CC   positions -475 or -147 of the DNA of the 5' flanking region adjacent to
CC   the CYP3A5 coding sequence. The variants are present in an activator
CC   protein-3 (AP-3) motif and/or a basic transcription element (BTE). The
CC   polymorphisms cause increased CYP3A5 gene expression and this has been
CC   linked to drug metabolic activity. Screening for the presence of variants
CC   can be used to identify subjects with a high or low drug metabolizing
CC   phenotype associated with cytochrome CYP3A5 expression. Primers are used
CC   which in addition to hybridizing to the site of interest, are capable of
CC   introducing a restriction site which is absent in either the wild type
CC   sequence or polymorphic variants. Restriction enzyme cleavage analysis
CC   can then be used to indicate the presence or absence of the variant. The
CC   methods are used to establish, before treatment with a drug, whether the
CC   drug will be effectively metabolized by the patient, to identify
CC   compounds and transcription factors that can bind to a DNA sequence
CC   encoding CYP3A5, diagnosing susceptibility to a disease which is caused
CC   by toxins or procarcinogens metabolized by CYP3A5 and for identifying
CC   mutagenic effects of a compound
XX
SQ   Sequence 16 BP; 6 A; 3 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             42.1%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 59;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAGTCCAG 27
              ||||||||||  |||
Db          2 GTACAGGGAGCACAG 16


RESULT 38
AAF45954/c
ID   AAF45954 standard; DNA; 15 BP.
XX
AC   AAF45954;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #793.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
```

```
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 2 A; 7 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             40.7%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   92.3%;  Pred. No. 67;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCCAGG 28
              |||||||||| ||
Db         14 CAGGGAGTCCTGG 2


RESULT 39
AAF45953/c
ID   AAF45953 standard; DNA; 15 BP.
XX
AC   AAF45953;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #792.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 2 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             40.7%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   92.3%;  Pred. No. 67;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCCAGG 28
              |||||||||| ||
Db         15 CAGGGAGTCCTGG 3


RESULT 40
AAF45955/c
ID   AAF45955 standard; DNA; 15 BP.
XX
AC   AAF45955;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #794.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
```

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PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 2 A; 8 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             40.7%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   92.3%;  Pred. No. 67;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCCAGG 28
               ||||||||||| ||
Db         13 CAGGGAGTCCTGG 1


RESULT 41
AAQ99935
ID   AAQ99935 standard; DNA; 16 BP.
XX
AC   AAQ99935;
XX
DT   07-MAY-1996  (first entry)
XX
DE   Human MTS1 RT-PCR primer, X2B.
XX
KW   Multiple tumour suppressor; E1-alpha; diagnosis; cancer; leukaemia;
KW   astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;
KW   gene therapy; chronic; ss.
XX
OS   Homo sapiens.
XX
PN   WO9525429-A1.
XX
PD   28-SEP-1995.
XX
PF   17-MAR-1995;   95WO-US003316.
XX
PR   18-MAR-1994;   94US-00214581.
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215088.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 1995-344401/44.
XX
PT   Wild-type multiple tumour suppressor (MTS) gene and mutant sequences -
PT   useful in diagnosis, prognosis and therapy of human cancer, e.g. melanoma
PT   or leukaemia.
XX
PS   Example 12; Page 68; 156pp; English.
XX
CC   The cDNA sequences encoding several multiple tumour suppressor (MTS)
CC   polypeptides have been isolated and sequenced, using various sequencing
CC   and amplification primers. The primer represented in this sequence was
CC   used to distinguish between two different promoters of MTS1, one alpha-
CC   specific and one beta-specific. MTS polypeptide-encoding cDNAs and
CC   mutants of these are useful for the diagnosis or prognosis of human
CC   cancer. Germ-line mutations of MTS cDNAs can be used for diagnosing
CC   predisposition to melanoma, leukaemia, astrocytoma, glioblastoma,
CC   lymphoma, glioma, Hodgkin's lymphoma, CLL and cancers of the pancreas,
CC   thyroid, ovary, uterus, testis, kidney, stomach and rectum. The wild-type
CC   gene is useful for gene therapy and MTS polypeptides may also be used for
CC   protein replacement therapy. Also the polypeptides or cells contg. an
CC   altered MTS gene are useful for screening for potential cancer
CC   therapeutics
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 83;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
               ||||| |||| || ||
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 42
AAT00727
ID   AAT00727 standard; DNA; 16 BP.
XX
AC   AAT00727;
XX
DT   08-MAY-1996  (first entry)
XX
DE   Multiple tumour suppressor 1 gene PCR primer.
XX
KW   Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;
KW   predisposition; melanoma; leukaemia; lymphoma; prognosis; pancreas;
KW   breast; thyroid; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9525813-A1.
XX
PD   28-SEP-1995.
XX
PF   17-MAR-1995;   95WO-US003537.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Skolnick MH,  Cannon-Albright LA,  Kamb A;
XX
DR   WPI; 1995-344626/44.
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```
XX
PT   Detecting polymorphism associated with cancer pre:disposition - also DNA,
PT   vectors and host cells e.g. for gene or protein replacement therapy and
PT   drug screening.
XX
PS   Example 12; Page 68; 148pp; English.
XX
CC   An individual can be diagnosed as having a predisposition to cancer by
CC   detecting an alteration in the wild type multiple tumour suppressor (MTS)
CC   gene, using gene probes which hybridise to the MTS1 gene exon 1 or exon
CC   1beta (amplified using the PCR primers AAT00724-27). The above assay can
CC   also be used in the diagnosis and prognosis of melanoma, lymphoma,
CC   leukaemia and pancreas, breast and thyroid cancers, etc
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 83;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
              ||||| |||| || ||
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 43
AAT69788
ID   AAT69788 standard; DNA; 16 BP.
XX
AC   AAT69788;
XX
DT   25-MAR-2003  (revised)
DT   10-SEP-1997  (first entry)
XX
DE   P16 promoter primer X2B.
XX
KW   Primer; polymerase chain reaction; PCR; amplification; P16; promoter; ss.
XX
OS   Synthetic.
XX
PN   US5624819-A.
XX
PD   29-APR-1997.
XX
PF   07-JUN-1995;   95US-00474177.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003537.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Cannon-Albright LA,  Kamb A,  Skolnick MH;
XX
DR   WPI; 1997-258217/23.
XX
PT   Human mutant multiple tumour suppressor gene sequences - for production
PT   of recombinant mutant polypeptide(s).
XX
PS   Example 12; Col 81-82; 72pp; English.
XX
CC   The present sequence is primer for the PCR amplification of the P16
CC   promoter. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 83;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
              ||||| |||| || ||
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 44
AAV53838
ID   AAV53838 standard; DNA; 16 BP.
XX
AC   AAV53838;
XX
DT   04-DEC-1998  (first entry)
XX
DE   Nucleotide sequence of PCR primer 9.
XX
KW   Multiple tumour suppressor; MTS; human; cancer; hybridisation;
KW   somatic mutation; gene therapy; PCR; primer; amplification; ss.
XX
OS   Synthetic.
XX
PN   US5801236-A.
XX
PD   01-SEP-1998.
XX
PF   07-JUN-1995;   95US-00480810.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003316.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 1998-494842/42.
XX
PT   Nucleic acids based on multiple tumour suppressor, MTS, sequences -
PT   useful as hybridisation probes, primers and recombinant production of MTS
PT   in the diagnosis and treatment of cancers related to MTS mutation(s).
XX
PS   Example 12; Col 51; 73pp; English.
XX
CC   This is the nucleotide sequence of a PCR primer used for amplification in
CC   the method of the invention involving the used of the multiple tumour
CC   suppressor (MTS) gene, to diagnose and treat cancer. The MTS gene is
CC   useful in the diagnosis and prognosis of human cancer, e.g. by standard
CC   nucleic hybridisation techniques, of patient samples. The mutated
CC   sequences are those that are present in somatic mutations of the gene in
CC   cancers. The vectors can be used for gene therapy strategies to replace
CC   function of mutated protein in patients. These can also be used to
CC   construct protein mimetics, also for therapeutic strategies. In addition
CC   the expression constructs can also be used for recombinant production of
CC   MTS. Recombinant MTS can be used to screen for drugs to be used for
CC   cancer therapy, and the protein itself may also be used to restore MTS
CC   function in a cell
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 83;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
              ||||| |||| || ||
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 45
AAV11257
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ID   AAV11257 standard; DNA; 16 BP.
XX
AC   AAV11257;
XX
DT   15-JUL-1998  (first entry)
XX
DE   Human MTS1 and MTS1E1-beta PCR primer X2B.
XX
KW   MTS1; MTS2; multiple tumour suppressor; diagnosis; cancer;
KW   germ-line mutation; familial melanoma locus; MLM; predisposition; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5739027-A.
XX
PD   14-APR-1998.
XX
PF   07-JUN-1995;   95US-00487033.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003316.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 1998-250421/22.
XX
PT   DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are useful
PT   for the diagnosis of cancers related to MTS1E1-beta mutation(s) and their
PT   treatment.
XX
PS   Example 12; Col 81-82; 72pp; English.
XX
CC   Primers AAV11256 and AAV11257 are used in the isolation of the human
CC   multiple tumour suppression proteins, MTS1 and MTS1E1-beta. The MTS gene
CC   locus is also referred to as the familial melanoma (MLM) gene locus,
CC   located on human chromosome 9p21. Germ line mutations in MTS genes can be
CC   used in the diagnosis of predisposition to cancers, e.g. melanoma,
CC   leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's
CC   lymphoma, CLL, and cancers of the pancreas, breast, thyroid, ovary,
CC   uterus, testis, kidney, stomach and rectum
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 83;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
              ||||| |||| || ||
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 46
AAV70602
ID   AAV70602 standard; DNA; 16 BP.
XX
AC   AAV70602;
XX
DT   20-MAR-2003  (revised)
DT   03-FEB-1999  (first entry)
XX
DE   PCR primer X2B for multiple tumour suppressor 2 gene.
XX
KW   Human; multiple tumour suppressor 2 gene; MTS2; cancer; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5843756-A.
XX
PD   01-DEC-1998.
XX
PF   28-JUL-1995;   95US-00508735.
XX
PR   17-MAR-1995;   95WO-US003316.
PR   07-JUN-1995;   95US-00487033.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Jiang P,  Kamb A,  Stone S;
XX
DR   WPI; 1999-044585/04.
XX
PT   Mouse multiple tumour suppressor gene segment - useful for primer design.
XX
PS   Example 14; Col 54; 80pp; English.
XX
CC   PCR primers AAV70600-02 were used to amplify a human multiple tumour
CC   suppressor 2 (MTS2) gene. The MTS2 gene nucleotide sequence can be used
CC   to design primers to detect abnormalities i.e. polymorphisms which may
CC   predispose towards malignancies such as melanoma, leukaemia, astrocytoma,
CC   lymphoma, glioma, as well as tumours of e.g. the breast, thyroid,
CC   pancreas, uterus and kidneys. (Updated on 20-MAR-2003 to correct PF
CC   field.) (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 83;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
              ||||| |||| || ||
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 47
AAA95654
ID   AAA95654 standard; DNA; 16 BP.
XX
AC   AAA95654;
XX
DT   14-FEB-2001  (first entry)
XX
DE   Human P16 promoter beta-specific primer X2B.
XX
KW   Cytostatic; human; multiple tumour suppressor 2; MTS2; diagnostic;
KW   cancer; gene therapy; protein replacement therapy; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6090578-A.
XX
PD   18-JUL-2000.
XX
PF   08-DEC-1997;   97US-00986515.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003316.
PR   07-JUN-1995;   95US-00480810.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
```

```
DR   WPI; 2000-514036/46.
XX
PT   Novel protein composition useful in protein replacement therapy for
PT   diagnosing and treating cancer comprises a specific weight percent of
PT   human multiple tumor suppressor 1 polypeptide.
XX
PS   Example 12; Col 49; 72pp; English.
XX
CC   The invention relates to the isolation of the gene encoding the human
CC   multiple tumour suppressor 1 (MTS1) (AAA95633). The MTS1 protein has a
CC   cytostatic activity and is used in protein replacement therapy. This
CC   sequence is a PCR primer used in the amplification of the beta-specific
CC   form of the P16 promoter. MTS1 is useful in diagnosing human cancers such
CC   as (ocular) melanoma, leukemia, astrocytoma, glioblastoma, lymphoma,
CC   glioma, Hodgkin's lymphoma, multiple myeloma, sarcoma, myosarcoma,
CC   cholangiocarcinoma, squamous cell carcinoma, CLL, and cancers of
CC   pancreas, breast, stomach, brain, prostate, bladder, thyroid, ovary,
CC   uterus, testis, kidney, colon and rectum. The MTS1 gene and protein is
CC   useful in gene therapy, protein replacement therapy and protein mimetic
CC   studies
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 83;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
              ||||| |||| || ||
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 48
AAZ48793
ID   AAZ48793 standard; cDNA; 16 BP.
XX
AC   AAZ48793;
XX
DT   21-MAR-2000  (first entry)
XX
DE   PCR primer for human MTS1E1beta coding sequence.
XX
KW   MTS; human; polymorphism detection; cancer predisposition; astrocytoma;
KW   Multiple Tumour Suppressor gene; melanoma; leukaemia; glioblastoma;
KW   lymphoma; glioma; Hodgkin's lymphoma; chronic lymphocytic leukaemia;
KW   therapy; MTS1E1beta; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US5989815-A.
XX
PD   23-NOV-1999.
XX
PF   29-APR-1997;   97US-00848251.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003537.
PR   07-JUN-1995;   95US-00474083.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Skolnick MH,  Cannon-Albright LA,  Kamb A;
XX
DR   WPI; 2000-070785/06.
XX
PT   Diagnosing a polymorphism associated with a predisposition for cancer.
XX
PS   Example 12; Col 48; 74pp; English.
XX
CC   This sequence is a PCR primer for DNA encoding human MTS1E1beta. The
CC   invention relates to a method for diagnosing a polymorphism associated
CC   with a predisposition to cancer by detecting a germ-line alteration of a
CC   wild-type Multiple Tumour Suppressor (MTS) gene or its expression
CC   products in a human sample. The method comprises detecting a germ-line
CC   alteration of a wild-type MTS gene or its expression products in a human
CC   sample, the alteration indicating a predisposition to at least one of the
CC   cancers. The cancer is selected from melanoma, leukaemia, astrocytoma,
CC   glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, chronic lymphocytic
CC   leukaemia (CLL), and cancers of the pancreas, breast, thyroid, ovary,
CC   uterus, testis, kidney, stomach and rectum. The method may be used as the
CC   basis for developing very important diagnostic tests capable of
CC   predicting the predisposition to cancer. The MTS gene is involved in the
CC   progression of multiple tumour types and may provide means for a general
CC   anti-cancer therapy by virtue of its ability to suppress tumour growth
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 83;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
              ||||| |||| || ||
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 49
AAZ39993
ID   AAZ39993 standard; DNA; 16 BP.
XX
AC   AAZ39993;
XX
DT   11-FEB-2000  (first entry)
XX
DE   PCR primer for human multiple tumour suppressor 1 coding sequence.
XX
KW   Multiple tumour suppressor; MTS2; human; diagnosis; Hodgkin's lymphoma;
KW   cancer predisposition; melanoma; leukaemia; lymphoma; glioma; MTS1;
KW   PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5994095-A.
XX
PD   30-NOV-1999.
XX
PF   07-JUN-1995;   95US-00486047.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003316.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 2000-038259/03.
XX
PT   Multiple tumor suppressor cDNA, useful for diagnosing or determining a
PT   predisposition to cancer.
XX
PS   Example 12; Col 48; 72pp; English.
XX
CC   This sequence represents a PCR primer for the human multiple tumour
CC   suppressor 1 (MTS1) coding sequence. The invention relates to the human
CC   MTS2 DNA and protein sequences. The DNA sequences are useful for
CC   diagnosing or determining a predisposition to cancers e.g. melanoma,
```

```
CC   leukaemia, lymphoma, glioma, Hodgkin's lymphoma and cancers of the
CC   pancreas, breast, thyroid, ovary, kidney, uterus and stomach
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 83;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
              ||||| |||| || ||
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 50
AAA39372
ID   AAA39372 standard; DNA; 16 BP.
XX
AC   AAA39372;
XX
DT   12-SEP-2000  (first entry)
XX
DE   Human P16 PCR primer SEQ ID NO:23.
XX
KW   Human; multiple tumour suppressor; MTS; somatic mutation; cancer;
KW   diagnosis; germ line mutation; gene therapy; cytostatic; melanoma;
KW   leukaemia; astrocytoma; glioblastoma; lymphoma; glioma;
KW   Hodgkin's lymphoma; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6060301-A.
XX
PD   09-MAY-2000.
XX
PF   14-JUL-1998;   98US-00115252.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003316.
PR   07-JUN-1995;   95US-00480810.
PR   08-DEC-1997;   97US-00986147.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 2000-349676/30.
XX
PT   New vector useful for gene therapy of cancer associated with mutation in
PT   tumor suppressor gene, comprises DNA sequence of multiple tumor
PT   suppressor gene.
XX
PS   Example 12; Col 48; 71pp; English.
XX
CC   The present invention describes a vector (I) comprising an isolated DNA
CC   sequence of a multiple tumour suppressor (MTS) gene having a
CC   polynucleotide sequence of the human MTS1E1-beta. (I) is useful for
CC   introducing wild-type MTS function to a cancerous or pre-cancerous cell
CC   which carries diminished or mutant MTS alleles for suppressing neoplastic
CC   growth of the recipient cells. (I) is also useful for increasing the
CC   level of expression of MTS gene even in tumour cells in which the mutant
CC   gene is expressed at a normal level but the gene product is not fully
CC   functional. A host cell transformed with (I) is useful as a model system
CC   to study cancer remission and drug treatment which promotes such
CC   remission. The present invention relates to somatic mutations and germ
CC   line mutations in the MTS gene and their use in the diagnosis and
CC   prognosis of human cancer e.g. melanoma, leukaemia, astrocytoma,
CC   glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, and cancers of the
CC   pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and
CC   rectum. The present sequence represents a PCR primer used in an example
CC   from the present invention
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 83;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
              ||||| |||| || ||
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 51
AAA11186
ID   AAA11186 standard; DNA; 16 BP.
XX
AC   AAA11186;
XX
DT   11-OCT-2000  (first entry)
XX
DE   Human multiple tumour suppressor 1 primer X2B.
XX
KW   Variant; human; multiple tumour suppressor; MTS; mutation; melanoma;
KW   cancer; diagnosis; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6037462-A.
XX
PD   14-MAR-2000.
XX
PF   22-JUL-1998;   98US-00120130.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003316.
PR   07-JUN-1995;   95US-00480810.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 2000-269915/23.
XX
PT   New mutants of the human multiple tumor suppressor gene, useful as
PT   diagnostic markers of cancer, contain specific base alterations or
PT   deletions.
XX
PS   Example 12; Col 48; 72pp; English.
XX
CC   The invention relates to variants (AAA11196-A11206) of the human multiple
CC   tumour suppressor 1 (MTS1) gene (AAA11165). The variants have the
CC   following changes relative to this sequence: A at any of positions 265,
CC   442, 330 and 329; T at any of positions 172, 238, 341 and 148 and
CC   deletions of nucleotides 290-294, 172-179 or 128-129. The variants are
CC   somatic mutations of MST1, indicative of predisposition to melanoma and
CC   many other cancers, so detecting them is useful for diagnosis, prognosis
CC   and monitoring of cancer (including prenatal analysis). Cells and animals
CC   that express the variants are useful as model systems for identifying
CC   potential anticancer agents. This sequence represents a primer used to
CC   screen for MTS1 E1beta initial mRNA expression levels
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 83;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy          10 CGTGTACAGGGAGTCC 25
               ||||| |||| || ||
Db           1 CGTGTCCAGGAAGCCC 16


RESULT 52
AAF58190
ID   AAF58190 standard; DNA; 16 BP.
XX
AC   AAF58190;
XX
DT   23-APR-2001  (first entry)
XX
DE   Primer #13.
XX
KW   Human; multiple tumour suppressor; MTS; cancer; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   US6180776-B1.
XX
PD   30-JAN-2001.
XX
PF   22-JUL-1998;   98US-00120129.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003316.
PR   07-JUN-1995;   95US-00486047.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 2001-158668/16.
XX
PT   Novel multiple tumor suppressor gene useful for diagnosing, prognosing
PT   and treating cancers, such as melanoma, leukemia, glioblastoma and
PT   Hodgkin's lymphoma.
XX
PS   Example 12; Col 48; 71pp; English.
XX
CC   The present invention relates to human multiple tumor suppressor-2 (MTS2)
CC   gene. The invention is useful for diagnosing, prognosing and treating
CC   cancers. It is also useful for screening drugs for cancer therapy and
CC   gene therapy
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 83;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          10 CGTGTACAGGGAGTCC 25
               ||||| |||| || ||
Db           1 CGTGTCCAGGAAGCCC 16


RESULT 53
AAS02583
ID   AAS02583 standard; DNA; 16 BP.
XX
AC   AAS02583;
XX
DT   29-AUG-2001  (first entry)
XX
DE   PCR primer X2B used in analysis of multiple tumour suppressor MTS1/2.
XX
KW   Human; multiple tumour suppressor; MTS1; MTS2; therapeutic; diagnostic;
KW   cancer; gene therapy; melanoma; leukaemia; astrocytoma; glioblastoma;
KW   lymphoma; glioma; Hodgkin's lymphoma; chronic lymphatic leukaemia;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6210949-B1.
XX
PD   03-APR-2001.
XX
PF   30-NOV-1998;   98US-00201139.
XX
PR   17-MAR-1995;   95WO-US003316.
PR   07-JUN-1995;   95US-00487033.
PR   28-JUL-1995;   95US-00508735.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Stone S,  Jiang P,  Kamb A;
XX
DR   WPI; 2001-280859/29.
XX
PT   New mouse multiple tumor suppressor gene, useful for diagnosing or
PT   prognosing human cancer or as gene therapy for treating cancer,
PT   particularly melanoma, leukemia, astrocytoma, lymphoma or cancers of the
PT   pancreas or breast.
XX
PS   Example 13; Col 51; 80pp; English.
XX
CC   The sequence represents PCR primer X2B used in analysis of multiple
CC   tumour suppressor MTS1 and MTS2. The MTS genes, and expression products,
CC   are useful for treating, diagnosing or prognosing human cancer. In
CC   particular, the MTS gene is useful for diagnosing a predisposition to or
CC   as a gene therapy for melanoma, leukaemia, astrocytoma, glioblastoma,
CC   lymphoma, glioma, Hodgkin's lymphoma, chronic lymphatic leukaemia (CLL),
CC   or cancers of the pancreas, breast, thyroid, ovary, uterus, testis,
CC   kidney, stomach or rectum. The gene may be used in both cancerous and pre
CC   -cancerous cells
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 83;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          10 CGTGTACAGGGAGTCC 25
               ||||| |||| || ||
Db           1 CGTGTCCAGGAAGCCC 16


RESULT 54
AAD04711
ID   AAD04711 standard; DNA; 16 BP.
XX
AC   AAD04711;
XX
DT   04-JUL-2001  (first entry)
XX
DE   Human MTS and MTS1E1beta sequence amplifying primer, X2B.
XX
KW   Human; multiple tumour suppressor; MTS1E1beta; cytostatic;
KW   germ line mutation; gene therapy; melanoma; leukaemia; astrocytoma; CLL;
KW   glioblastoma; lymphoma; glioma; Hodgkin's lymphoma; cancer; rectum;
KW   pancreas; breast; thyroid; ovary; uterus; testis; kidney; stomach;
KW   somatic mutation; MTS; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6218146-B1.
XX
PD   17-APR-2001.
XX
PF   22-JUL-1998;   98US-00120131.
XX
PR   18-MAR-1994;   94US-00214582.
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PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003316.
PR   07-JUN-1995;   95US-00486047.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 2001-289831/30.
XX
PT   Novel multiple tumor suppressor proteins useful for diagnosis and
PT   prognosis of human cancer and for screening drugs for cancer treatment.
XX
PS   Example 13; Col 52; 71pp; English.
XX
CC   The invention relates to somatic and germ line mutations in the multiple
CC   tumour suppressor (MTS) gene in human cancer. The invention also relates
CC   to therapy of human cancer which have a mutation in the MTS gene,
CC   including gene therapy, protein replacement therapy, and protein
CC   mimetics. The MTS sequences are useful for diagnosing predisposition to
CC   human cancer or for diagnosing and prognosing human cancers such as
CC   melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,
CC   Hodgkin's lymphoma, CLL and cancers of pancreas, breast, thyroid, ovary,
CC   uterus, testis, kidney, stomach and rectum. They are also used for
CC   screening drugs for cancer treatment. The present sequence is primer, X2B
CC   used for amplifying human MTS and MTS1E1beta sequence
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 83;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
               ||||| |||| || ||
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 55
AAC83090
ID   AAC83090 standard; DNA; 16 BP.
XX
AC   AAC83090;
XX
DT   23-FEB-2001  (first entry)
XX
DE   Primer X2B used in the invention.
XX
KW   MTS; Multiple Tumour Suppressor; cancer; antibody; ss.
XX
OS   Homo sapiens.
XX
PN   US6140473-A.
XX
PD   31-OCT-2000.
XX
PF   22-JUL-1998;   98US-00120128.
XX
PR   18-MAR-1994;   94US-00214582.
PR   18-MAR-1994;   94US-00215086.
PR   18-MAR-1994;   94US-00215087.
PR   14-APR-1994;   94US-00227369.
PR   01-JUN-1994;   94US-00251938.
PR   17-MAR-1995;   95WO-US003316.
PR   07-JUN-1995;   95US-00486047.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Kamb A;
XX
DR   WPI; 2001-014867/02.
XX
PT   New multiple tumor suppressor 2-specific antibodies useful for detecting
PT   differences in the absence of the peptides or mutant gene products, or
PT   for screening tissues.
XX
PS   Example 12; Col 48; 71pp; English.
XX
CC   The present invention relates to an antibody or its fragment that
CC   specifically binds to a human multiple tumour suppressor (MTS). The
CC   invention is useful for detecting differences in the absence of MTS
CC   peptides, to screen a tissue or to detect mutant MTS gene products. The
CC   antibodies will immunoprecipitate MTS proteins from solution as well as
CC   react with MTS protein on Western or immunoblots of polyacrylamide gels
XX
SQ   Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 83;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
               ||||| |||| || ||
Db          1 CGTGTCCAGGAAGCCC 16


RESULT 56
ADC98469/c
ID   ADC98469 standard; DNA; 16 BP.
XX
AC   ADC98469;
XX
DT   01-JAN-2004  (first entry)
XX
DE   NOT304 polymorphism marker PCR primer B primer seq.
XX
KW   low bone mineral density; BMD; bone damage; polymorphism; osteoporosis;
KW   single nucleotide polymorphism; SNP; PCR primer; ss; human.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003054218-A2.
XX
PD   03-JUL-2003.
XX
PF   19-DEC-2002; 2002WO-US040948.
XX
PR   20-DEC-2001; 2001US-0342711P.
PR   04-NOV-2002; 2002US-0423559P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Jones KA,  Valdes A,  Townley DJ,  Mangion J,  Galwey N,  Bennett S;
PI   Mckay I,  Schafer A;
XX
DR   WPI; 2003-559156/52.
XX
PT   Determining whether an individual is predisposed to susceptibility to low
PT   bone mineral density (BMD) and/or bone damage, involves identifying
PT   polymorphisms in associated genes.
XX
PS   Example 8; Page 238; 246pp; English.
XX
CC   The present invention describes a method of determining whether an
CC   individual is predisposed to susceptibility to low bone mineral density
CC   (BMD) and/or bone damage comprising identifying whether the individual
CC   has at least one polymorphism in a polynucleotide encoding a protein,
CC   where the polynucleotide is one of 81 200-500 nucleotide sequences (S1,
CC   see ADC98235 to ADC98315). An agent identified in an method from the
CC   present invention which can be used for the prevention or treatment of a
CC   disease resulting in susceptibility to low BMD and/or bone damage is
CC   useful in the manufacture of a medicament for use in modulating the
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CC   susceptibility to low BMD and/or bone damage. The disease associated with
CC   low BMD and/or bone damage is osteoporosis. The present PCR primer
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 16 BP; 2 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 83;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          11 GTGTACAGGGAGTCCA 26
               | || ||| |||||||
Db          16 GAGTCCAGCGAGTCCA 1


RESULT 57
AAF07226
ID   AAF07226 standard; DNA; 17 BP.
XX
AC   AAF07226;
XX
DT   16-FEB-2001  (first entry)
XX
DE   Hammerhead ribozyme substrate #3483.
XX
KW   Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW   interferon alpha; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061729-A2.
XX
PD   19-OCT-2000.
XX
PF   11-APR-2000; 2000WO-US009721.
XX
PR   12-APR-1999;   99US-0129390P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Zwick M,  Pavco P,  Mcswiggen J;
XX
DR   WPI; 2000-647423/62.
XX
PT   Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT   useful for producing e.g. granulocyte colony stimulating factor protein,
PT   interferon alpha and erythropoietin.
XX
PS   Claim 54; Page 136; 164pp; English.
XX
CC   The present invention relates to enzymatic and antisense nucleic acid
CC   molecules that act as inhibitors of the expression of repressor genes
CC   encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC   factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC   Inhibition of the repressors removes prevents inhibition (and
CC   consequently increases expression of) genes involved in the production of
CC   erythropoietin, granulocyte colony stimulating factor protein and
CC   interferon alpha
XX
SQ   Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 91;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy           7 CTACGTGTACAGGGAG 22
               |||| |||||  ||||
Db           1 CTACATGTACCAGGAG 16


RESULT 58
ABA80105
ID   ABA80105 standard; DNA; 17 BP.
XX
AC   ABA80105;
XX
DT   24-JAN-2002  (first entry)
XX
DE   HBA2 mutation correcting oligonucleotide SEQ ID NO: 2951.
XX
KW   Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
KW   retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
KW   cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
KW   adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
KW   haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
KW   mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
KW   familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
KW   UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
KW   Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
KW   antilipemic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200173002-A2.
XX
PD   04-OCT-2001.
XX
PF   27-MAR-2001; 2001WO-US009761.
XX
PR   27-MAR-2000; 2000US-0192176P.
PR   27-MAR-2000; 2000US-0192179P.
PR   01-JUN-2000; 2000US-0208538P.
PR   30-OCT-2000; 2000US-0244989P.
XX
PA   (UYDE ) UNIV DELAWARE.
XX
PI   Kmiec EB,  Gamper HB,  Rice MC;
XX
DR   WPI; 2001-639230/73.
XX
PT   Oligonucleotide for targeted alterations of genetic sequences and for
PT   treating cystic fibrosis, comprises at least one mismatch and chemical
PT   modification.
XX
PS   Claim 7; Page 208; 294pp; English.
XX
CC   The present invention provides single-stranded oligonucleotides which can
CC   be used for the targeted alteration of genomic sequences, where the
CC   oligonucleotide has at least one mismatch compared with the genomic
CC   sequence to be altered. In particular, these sequences are directed at
CC   the following genes: adenosine deaminase, p53, beta-globin,
CC   retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
CC   (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
CC   1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
CC   apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC   (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
CC   presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
CC   such as cancer, adenosine deaminase deficiency, cystic fibrosis,
CC   haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
CC   Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
CC   various syndromes. The present sequence is one of the gene correcting
CC   oligonucleotides of the invention
XX
SQ   Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 91;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy           9 ACGTGTACAGGGAGTC 24
               || ||| |||||||  |
Db           1 ACTTGTCCAGGGAGGC 16


RESULT 59
ABA80104/c
```

```
ID   ABA80104 standard; DNA; 17 BP.
XX
AC   ABA80104;
XX
DT   24-JAN-2002  (first entry)
XX
DE   HBA2 mutation correcting oligonucleotide SEQ ID NO: 2950.
XX
KW   Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
KW   retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
KW   cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
KW   adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
KW   haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
KW   mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
KW   familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
KW   UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
KW   Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
KW   antilipemic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200173002-A2.
XX
PD   04-OCT-2001.
XX
PF   27-MAR-2001; 2001WO-US009761.
XX
PR   27-MAR-2000; 2000US-0192176P.
PR   27-MAR-2000; 2000US-0192179P.
PR   01-JUN-2000; 2000US-0208538P.
PR   30-OCT-2000; 2000US-0244989P.
XX
PA   (UYDE ) UNIV DELAWARE.
XX
PI   Kmiec EB,  Gamper HB,  Rice MC;
XX
DR   WPI; 2001-639230/73.
XX
PT   Oligonucleotide for targeted alterations of genetic sequences and for
PT   treating cystic fibrosis, comprises at least one mismatch and chemical
PT   modification.
XX
PS   Claim 7; Page 208; 294pp; English.
XX
CC   The present invention provides single-stranded oligonucleotides which can
CC   be used for the targeted alteration of genomic sequences, where the
CC   oligonucleotide has at least one mismatch compared with the genomic
CC   sequence to be altered. In particular, these sequences are directed at
CC   the following genes: adenosine deaminase, p53, beta-globin,
CC   retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
CC   (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
CC   1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
CC   apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC   (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
CC   presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
CC   such as cancer, adenosine deaminase deficiency, cystic fibrosis,
CC   haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
CC   Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
CC   various syndromes. The present sequence is one of the gene correcting
CC   oligonucleotides of the invention
XX
SQ   Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 91;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          9 ACGTGTACAGGGAGTC 24
              || ||| ||||||| |
Db         17 ACTTGTCCAGGGAGGC 2


RESULT 60
ADB00357
ID   ADB00357 standard; DNA; 17 BP.
XX
AC   ADB00357;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ3 scanning oligonucleotide SEQ ID 1343.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 1343; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 2 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 91;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGTCC 25
              ||||| ||| |||| |
Db          1 CGTGTGCAGCGAGTGC 16


RESULT 61
ABZ61654
ID   ABZ61654 standard; RNA; 17 BP.
XX
AC   ABZ61654;
XX
DT   21-MAR-2003  (first entry)
XX
DE   Human H-Ras DNAzyme target #445.
```

```
XX
KW   Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW   enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW   anti-rheumatic; cancer; AIDS; ss.
XX
OS   Homo sapiens.
XX
PN   WO200297114-A2.
XX
PD   05-DEC-2002.
XX
PF   29-MAY-2002; 2002WO-US016840.
XX
PR   29-MAY-2001; 2001US-0294140P.
PR   06-JUN-2001; 2001US-0296249P.
PR   10-SEP-2001; 2001US-0318471P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J;
XX
DR   WPI; 2003-140484/13.
XX
PT   Novel short interfering RNA and enzymatic nucleic acid useful for
PT   treating cancer, modulates the expression of a nucleic acid encoding
PT   HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS   Claim 58; Page 119; 185pp; English.
XX
CC   The invention relates to a novel short interfering RNA (siRNA) nucleic
CC   acid molecule or an enzymatic nucleic acid molecule, that modulates
CC   expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC   human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC   acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC   rheumatic activity. The nucleic acid molecules are useful for reducing
CC   HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC   also useful for treating breast, ovarian, colorectal, lung, prostate,
CC   bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC   shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC   ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC   ribozymes of the invention
XX
SQ   Sequence 17 BP; 5 A; 6 C; 5 G; 0 T; 1 U; 0 Other;

  Query Match             40.0%;  Score 11.2;  DB 1;  Length 17;
  Best Local Similarity   75.0%;  Pred. No. 91;
  Matches   12;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGGGAG 22
              | ||  |:||||||||
Db          1 CCACCAGUACAGGGAG 16


RESULT 62
AAX31582/c
ID   AAX31582 standard; DNA; 15 BP.
XX
AC   AAX31582;
XX
DT   21-MAY-1999  (first entry)
XX
DE   Tag sequence of a transcript increased in pancreatic cancer.
XX
KW   Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
KW   diagnosis; prognosis; treatment; ss.
XX
OS   Homo sapiens.
XX
PN   WO9853319-A2.
XX
PD   26-NOV-1998.
XX
PF   20-MAY-1998;   98WO-US010277.
XX
PR   21-MAY-1997;   97US-0047352P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1999-070161/06.
XX
PT   Use of isolated gene transcripts - useful for developing products for the
PT   diagnosis, prognosis and treatment of cancers, particularly colon and
PT   pancreatic cancer.
XX
PS   Claim 13; Page 62; 120pp; English.
XX
CC   AAX30947-31815 represent tag sequences of transcripts that are
CC   differentially expressed in colorectal cancer, in pancreatic cancer, or
CC   in both. The tag sequences can be used to identify genes by matching the
CC   tag to a gen data base member, or by using the tag sequences as probes to
CC   isolate unidentified genes from cDNA libraries. The tag sequences can
CC   also be used in a method for diagnosing colon or pancreatic cancer in a
CC   sample suspected of being neoplastic. The method comprises comparing the
CC   level of at least one transcript in a first sample of a tissue to a
CC   second sample, where the first sample is a colonic tissue suspected of
CC   being neoplastic and the second sample is a normal human colonic tissue.
CC   The transcript is identified by a tag selected from AAX30947-31815. The
CC   methods of the invention can be used in the diagnosis, prognosis and
CC   treatment of cancer
XX
SQ   Sequence 15 BP; 2 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             38.6%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 94;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAGTCCAGG 28
              |||| ||||||| |
Db         14 ACAGAGAGTCCATG 1


RESULT 63
AAZ62510
ID   AAZ62510 standard; RNA; 15 BP.
XX
AC   AAZ62510;
XX
DT   28-MAR-2000  (first entry)
XX
DE   Substrate for HH ribozyme HCV-2043 which cleaves HCV RNA at nt. 2043.
XX
KW   Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW   cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW   autoimmune disease; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO9955847-A2.
XX
PD   04-NOV-1999.
XX
PF   26-APR-1999;   99WO-US009027.
XX
PR   27-APR-1998;   98US-0083217P.
PR   18-SEP-1998;   98US-0100842P.
PR   25-FEB-1999;   99US-00257608.
PR   23-MAR-1999;   99US-00274553.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Mcswiggen JA,  Roberts E,  Pavco PA,  Macejak D;
XX
DR   WPI; 2000-062023/05.
XX
```

```
PT   Novel ribozymes for the treatment of diseases and conditions related to
PT   hepatitis C infection.
XX
PS   Claim 1; Page 54; 123pp; English.
XX
CC   The present sequence represents the preferred target sequence of an
CC   enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC   the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC   the descriptor line. The HCV sequence was screened for optimal ribozyme
CC   target sites using a computer folding algorithm and regions of the mRNA
CC   which did not form secondary folding structures and contained potential
CC   ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC   target these sites and their activities optimised by either varying the
CC   length of the binding arms or by modification to prevent degradation by
CC   nucleases. The ribozymes of the invention inhibit gene expression and/or
CC   viral replication, and are used to treat diseases associated with
CC   Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC   hepatocellular carcinoma. The ribozymes may be used in combination with
CC   interferon to treat HCV infection, other infectious diseases, autoimmune
CC   diseases, and cancer
XX
SQ   Sequence 15 BP; 2 A; 6 C; 5 G; 0 T; 2 U; 0 Other;

  Query Match             38.6%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   71.4%;  Pred. No. 94;
  Matches   10;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GGGCCCTACGTGTA 15
              ||||||: ||:| |
Db          1 GGGCCCUCCGUGCA 14


RESULT 64
AAH74110
ID   AAH74110 standard; DNA; 15 BP.
XX
AC   AAH74110;
XX
DT   17-DEC-2001  (first entry)
XX
DE   Primer #7 used in identification of gene transcripts.
XX
KW   Primer; DGE; differential gene expression; gene identification; ss.
XX
OS   Unidentified.
XX
PN   EP1113382-A1.
XX
PD   04-JUL-2001.
XX
PF   27-DEC-1999;   99EP-00126017.
XX
PR   27-DEC-1999;   99EP-00126017.
XX
PA   (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI   Colinge J,  Feger G;
XX
DR   WPI; 2001-443815/48.
XX
PT   Identifying gene transcripts, involves generating first set of raw
PT   sequences by sequencing biological material, isolating first ditags and
PT   first tags, determining abundance of first tags, reducing sequencing
PT   errors.
XX
PS   Disclosure; Fig 10; 104pp; English.
XX
CC   The invention relates to a method of identifying gene transcripts, which
CC   involves generating at least a first set of raw sequences (RS) by
CC   sequencing at least a first type of biological material, isolating first
CC   ditags (DT) from RS, isolating first tags (T1) from DT, determining the
CC   abundance of T1 and identifying T1, and then reducing the amount of
CC   sequencing errors using a statistical model for sequencing errors to be
CC   applied to T1. The method is useful for the identification of gene
CC   transcripts such as RNA or their corresponding cDNAs, and also for
CC   collecting information from several cell types, e.g. with reference to
CC   DGE (differential gene expression) studies. The method has improved
CC   efficiency in the treatment of errors, greatly reduces the error rate of
CC   the tags by estimating the error rate and consequently rejecting
CC   dangerous tags. It provides an easy way for consulting the identified
CC   tags by use of an improved graphical interface. Sequencing error is
CC   reduced by applying a statistical model. A measure of correctness of
CC   identification is provided, by allowing the user to confirm the
CC   identification through use of more than one database. The method provides
CC   not only a text form which is richer than other interfaces for similar
CC   data in terms of information about identified tags, but also an improved
CC   graphical interface which allows an easy interpretation of the results
CC   and an easy access to e.g. the KEGG (undefined) pathway. The present
CC   sequence represents primer #7 used in the method of the invention
XX
SQ   Sequence 15 BP; 5 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             38.6%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 94;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          10 CGTGTACAGGGAGT 23
               | |||||||| |||
Db           1 CATGTACAGGAAGT 14


RESULT 65
ABS97123/c
ID   ABS97123 standard; DNA; 15 BP.
XX
AC   ABS97123;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Human CYP4501A1 promoter 1A sequencing primer #1.
XX
KW   Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; PCR;
KW   cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
KW   adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW   aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW   cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW   epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW   glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW   HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW   NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;
KW   UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW   UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW   multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW   multidrug resistance associated protein 3; cancer; prostate;
KW   acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW   altered drug metabolism; cardiovascular function; colorectal tumour;
KW   central nervous system; pulmonary; immunological.
XX
OS   Homo sapiens.
XX
PN   WO200257410-A2.
XX
PD   25-JUL-2002.
XX
PF   28-NOV-2001; 2001WO-US044838.
XX
PR   28-NOV-2000; 2000US-00724389.
XX
PA   (DNAS-) DNA SCI LAB INC.
XX
PI   Guida M,  Hall J;
XX
DR   WPI; 2002-698522/75.
XX
PT   Isolated nucleic acid molecules having polymorphisms in known human genes
PT   e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
```

```
PT   for locating, identifying and characterizing the genes responsible for
PT   disorder-related traits.
XX
PS   Example 1; Page 99; 714pp; English.
XX
CC   This invention relates to the sequence of an isolated nucleic acid
CC   molecule comprising at least one base variation from that of a known
CC   human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC   cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
CC   aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC   (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding
CC   inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC   protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC   transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
CC   transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC   sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC   (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC   transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
CC   (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC   (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
CC   receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC   The polymorphisms in the human genes cited in the invention are useful as
CC   genetic linkage markers for locating and characterising the genes that
CC   are responsible for specific traits within the genome and eventually
CC   identifying the genes responsible for a variety of disorder-related
CC   traits as a result of their e.g., overexpression, constitutive
CC   expression, mutation or underexpression, which may be used in diagnosing
CC   and/or treating the disorders. The nucleic acid molecules comprising the
CC   polymorphic sequences contained in CYP4501A1, CYPP4501A2, CYP4502E1,
CC   ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC   MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC   metabolism. The polymorphic sequences contained in CYP4501A1, CYPP4501A2,
CC   AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC   susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC   used to screen for altered cardiovascular function, in COX2 for altered
CC   susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
CC   nervous system function, in FLAP and HNMT for altered pulmonary,
CC   immunological or haematological function, in KLK2 for altered serine
CC   protease activity in the prostate, in LTF for altered immunological or
CC   haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC   peripheral nervous system function. The present sequence represents a PCR
CC   primer used to amplify the sequences of the invention
XX
SQ   Sequence 15 BP; 3 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             38.6%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 94;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          15 ACAGGGAGTCCAGG 28
               ||||||  ||||||
Db          15 ACAGGGTTTCCAGG 2


RESULT 66
ABK32536/c
ID   ABK32536 standard; DNA; 15 BP.
XX
AC   ABK32536;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human pancreatic cancer SAGE tag #88.
XX
KW   Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
KW   serial analysis of gene expression; diagnostic; prognostic; probe;
KW   cancer marker; ss.
XX
OS   Homo sapiens.
XX
PN   US6333152-B1.
XX
PD   25-DEC-2001.
XX
PF   20-MAY-1998;   98US-00081646.
XX
PR   20-MAY-1998;   98US-00081646.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW,  Zhang L,  Zhou W;
XX
DR   WPI; 2002-153821/20.
XX
PT   New human nucleic acid containing specific SAGE tags, useful as
PT   diagnostic markers for cancer, also derived probes.
XX
PS   Disclosure; Col 73; 161pp; English.
XX
CC   The invention relates to an isolated, purified human nucleic acid (I)
CC   that has the same sequence as a mRNA found in humans and is a SAGE
CC   (serial analysis of gene expression) tag comprising a single stranded
CC   probe containing at least 10 consecutive nucleotides. SAGE tags, are
CC   diagnostic and prognostic markers of cancer, especially of the colon and
CC   pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
CC   SAGE tags of the invention
XX
SQ   Sequence 15 BP; 2 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             38.6%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 94;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          15 ACAGGGAGTCCAGG 28
               ||||  |||||||  |
Db          14 ACAGAGAGTCCATG 1


RESULT 67
ABX00361
ID   ABX00361 standard; RNA; 15 BP.
XX
AC   ABX00361;
XX
DT   23-DEC-2002  (first entry)
XX
DE   Hepatitis C virus substrate #143 for HCV hammerhead ribozyme #143.
XX
KW   Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW   HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW   liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW   type I interferon; interferon alpha; interferon beta; cytostatic;
KW   interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW   substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS   Hepatitis C virus.
XX
PN   US2002082225-A1.
XX
PD   27-JUN-2002.
XX
PF   23-MAR-1999;   99US-00274553.
XX
PR   23-MAR-1999;   99US-00274553.
XX
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J A.
PA   (ROBE/) ROBERTS B.
PA   (PAVC/) PAVCO P A.
PA   (MACE/) MACEJACK D.
XX
PI   Blatt L,  Mcswiggen JA,  Roberts B,  Pavco PA,  Macejack D;
XX
DR   WPI; 2002-617759/66.
XX
PT   New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
```

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PT   replication and are useful to treat hepatitis C virus infections and
PT   cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS   Claim 1; Page 25; 80pp; English.
XX
CC   The present invention relates to enzymatic nucleic acids which
CC   specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC   enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC   (HP) motif where the binding arms comprise sequences complementary to one
CC   of the substrate sequences defined in the specification. The HCV
CC   ribozymes are useful for modulating the expression and/or replication of
CC   HCV. They can be used to treat cirrhosis, liver failure and/or
CC   hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC   a condition associated with HCV infection in conjunction with one or more
CC   other drug therapies, particularly type I interferon, especially
CC   interferon alpha, beta or gamma or consensus interferon. The present
CC   sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC   Some of the sequence data for this patent did not form part of the
CC   printed specification. The complete sequence data for this patent was
CC   obtained in electronic format directly from the USPTO web site at
CC   seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ   Sequence 15 BP; 2 A; 6 C; 5 G; 0 T; 2 U; 0 Other;

  Query Match             38.6%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   71.4%;  Pred. No. 94;
  Matches   10;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GGGCCCTACGTGTA 15
              ||||||: ||:| |
Db          1 GGGCCCUCCGUGCA 14


RESULT 68
ABI00908/c
ID   ABI00908 standard; DNA; 12 BP.
XX
AC   ABI00908;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 300881 for detecting SNP TSC0019231.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 300881; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             37.1%;  Score 10.4;  DB 1;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 83;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAGT 23
               |||| |||||||
Db          12 TGTAGAGGGAGT 1


RESULT 69
ABC37718
ID   ABC37718 standard; DNA; 13 BP.
XX
AC   ABC37718;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 37735 for detecting SNP TSC0011735.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 37735; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             37.1%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 94;
```

```
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              |||||||| |||
Db          2 TACGTGTATAGG 13


RESULT 70
ABC37719/c
ID   ABC37719 standard; DNA; 13 BP.
XX
AC   ABC37719;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 37736 for detecting SNP TSC0011735.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 37736; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             37.1%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 94;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              |||||||| |||
Db         12 TACGTGTATAGG 1


RESULT 71
AAF47954/c
ID   AAF47954 standard; DNA; 15 BP.
XX
AC   AAF47954;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP3 oligonucleotide #1374.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 7; Page 53; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 8 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             37.1%;  Score 10.4;  DB 1;  Length 15;
  Best Local Similarity   91.7%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
              ||||| ||||||
Db         14 TGTACGGGGAGT 3


RESULT 72
AAF46048/c
ID   AAF46048 standard; DNA; 15 BP.
XX
AC   AAF46048;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #887.
XX
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KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 8 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             37.1%;  Score 10.4;  DB 1;  Length 15;
  Best Local Similarity   91.7%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
              ||| ||||||||
Db         12 TGTGCAGGGAGT 1


RESULT 73
AAF46045/c
ID   AAF46045 standard; DNA; 15 BP.
XX
AC   AAF46045;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #884.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             37.1%;  Score 10.4;  DB 1;  Length 15;
  Best Local Similarity   91.7%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
              ||| ||||||||
Db         15 TGTGCAGGGAGT 4


RESULT 74
AAF46046/c
ID   AAF46046 standard; DNA; 15 BP.
XX
AC   AAF46046;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #885.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
```

```
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             37.1%;  Score 10.4;  DB 1;  Length 15;
  Best Local Similarity   91.7%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAGT 23
               ||| ||||||||
Db          14 TGTGCAGGGAGT 3


RESULT 75
AAF46047/c
ID   AAF46047 standard; DNA; 15 BP.
XX
AC   AAF46047;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #886.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 7 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             37.1%;  Score 10.4;  DB 1;  Length 15;
  Best Local Similarity   91.7%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAGT 23
               ||| ||||||||
Db          13 TGTGCAGGGAGT 2


RESULT 76
AAF47955/c
ID   AAF47955 standard; DNA; 15 BP.
XX
AC   AAF47955;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP3 oligonucleotide #1375.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
```

```
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 7; Page 53; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 7 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             37.1%;  Score 10.4;  DB 1;  Length 15;
  Best Local Similarity   91.7%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
               ||||| ||||||
Db         13 TGTACGGGGAGT 2


RESULT 77
AAF47956/c
ID   AAF47956 standard; DNA; 15 BP.
XX
AC   AAF47956;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP3 oligonucleotide #1376.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 7; Page 53; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 6 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             37.1%;  Score 10.4;  DB 1;  Length 15;
  Best Local Similarity   91.7%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
               ||||| ||||||
Db         12 TGTACGGGGAGT 1


RESULT 78
AAF47953/c
ID   AAF47953 standard; DNA; 15 BP.
XX
AC   AAF47953;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP3 oligonucleotide #1373.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
```

```
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 7; Page 53; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 9 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             37.1%;  Score 10.4;  DB 1;  Length 15;
  Best Local Similarity   91.7%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
               ||||| ||||||
Db         15 TGTACGGGGAGT 4


RESULT 79
AAF45952/c
ID   AAF45952 standard; DNA; 15 BP.
XX
AC   AAF45952;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #791.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 2 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             37.1%;  Score 10.4;  DB 1;  Length 15;
  Best Local Similarity   91.7%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTCCAGG 28
               ||||||||| ||
Db         15 AGGGAGTCCTGG 4


RESULT 80
AAF45956/c
ID   AAF45956 standard; DNA; 15 BP.
XX
AC   AAF45956;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #795.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
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```
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 7 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             37.1%;  Score 10.4;  DB 1;  Length 15;
  Best Local Similarity   91.7%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          16 CAGGGAGTCCAG 27
               ||||||||||  |
Db          12 CAGGGAGTCCTG 1


RESULT 81
ABQ88645
ID   ABQ88645 standard; DNA; 15 BP.
XX
AC   ABQ88645;
XX
DT   23-SEP-2002  (first entry)
XX
DE   Human CFL1 ASO probe #4.
XX
KW   Human; cofilin 1; CFL1; gene therapy; antisense gene therapy;
KW   immunological disorder; ASO; allele-specific oligonucleotide; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200194376-A1.
XX
PD   13-DEC-2001.
XX
PF   11-JUN-2001; 2001WO-US018815.
XX
PR   09-JUN-2000; 2000US-0210884P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Anastasio AE,  Duda A,  Kliem SE,  Koshy B,  Sausker EA;
XX
DR   WPI; 2002-566437/60.
XX
PT   Novel genetic variants of human cofilin 1, CFL1 gene for studying
PT   expression, function of the gene and expressing CFL1 protein useful in
PT   identifying drugs to treat immunological disorders.
XX
PS   Claim 17; Page 13; 84pp; English.
XX
CC   The invention relates to a novel polynucleotide sequence which is a
CC   polymorphic variant of a reference sequence for the cofilin 1 (non-
CC   muscle) (CFL1) gene or its fragment, or a polymorphic variant of a
CC   reference sequence for a CFL1 cDNA or its fragment. The polynucleotide of
CC   the invention may have a use in gene therapy, and in antisense gene
CC   therapy. The polynucleotide is useful for studying the expression and
CC   function of CFL1 and expressing CFL1 protein for use in screening for
CC   candidate drugs to treat diseases related to CFL1 activity. The
CC   polymorphism and haplotype data are useful for validating whether CFL1 is
CC   a suitable target for drugs to treat immunological disorders, screening
CC   for such drugs and reducing bias in clinical trials of such drugs. The
CC   present sequence represents one of a set of allele-specific
CC   oligonucleotide (ASO) probes used in the invention to detect
CC   polymorphisms in the CFL1 gene
XX
SQ   Sequence 15 BP; 2 A; 6 C; 2 G; 4 T; 0 U; 1 Other;

  Query Match             37.1%;  Score 10.4;  DB 1;  Length 15;
  Best Local Similarity   78.6%;  Pred. No. 1.2e+02;
  Matches   11;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           5 CCCTACGTGTACAG 18
               ||||||:|| || |
Db           2 CCCTACRTGCACTG 15


RESULT 82
AAA52434/c
ID   AAA52434 standard; DNA; 15 BP.
XX
AC   AAA52434;
XX
DT   18-SEP-2000  (first entry)
XX
DE   TdT-expressing Ramos cell VH insertion+deletion mutation, F264.
XX
KW   Lymphoid cell; antibody producing cell; Ramos cell; immunoglobulin M;
KW   IgM; V gene diversity; directed constitutive hypermutation;
KW   target sequence diversification; terminal deoxynucleotidyl transferase;
KW   TdT; clonal expansion; selection; heavy chain variable region; VH;
KW   mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200022111-A1.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-GB003358.
XX
PR   09-OCT-1998;   98GB-00022104.
PR   19-JAN-1999;   99GB-00001141.
PR   09-JUN-1999;   99GB-00013435.
XX
PA   (MEDI-) MEDICAL RES COUNCIL.
XX
PI   Sale JE,  Neuberger MS,  Cumbers SJ;
XX
DR   WPI; 2000-317971/27.
XX
PT   Lymphoid cell line preparation useful for producing gene products having
PT   desired activity, involves screening and selecting cells having ongoing
PT   target sequence diversification and higher mutation rates.
XX
PS   Example 4; Fig 6; 69pp; English.
XX
CC   The invention relates to a method of preparing a lymphoid cell line
CC   capable of capable of directed constitutive hypermutation of a target
CC   nucleic acid region. The method comprises screening a cell population for
CC   ongoing target sequence diversification and selecting a cell in which the
CC   rate of target nucleic acid mutation exceeds that of other nucleic acid
CC   mutation by a factor of 100 or more. The invention also relates to a
CC   method for preparing a gene product with a desired activity, comprising
CC   expressing a nucleic acid encoding the target gene operably linked to a
CC   sequence which directs hypermutation e.g., terminal deoxynucleotidyl
CC   transferase (TdT), in the lymphoid cell line, and identifying a cell or
CC   cells which express a mutated gene product with the desired activity. One
CC   or more clonal populations of the identified cells is established, and
CC   cells with an improved activity of interest are selected. These steps may
CC   be iteratively repeated until a gene product with a desired of activity
CC   is obtained. The cell lines prepared according to the method of the
CC   invention are used for directed constitutive hypermutation of a nucleic
CC   acid region in the preparation of a gene product, preferably an enzyme or
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CC   an immunoglobulin (Ig) with a desired activity. In the exemplifications
CC   of the invention, IgM-secreting Ramos cells were selected for use as they
CC   undergo hypermutation during clonal expansion. This was determined on the
CC   basis of the amount of diversity in the heavy chain variable region (VH).
CC   Sequences AAA52366-A52434 represent fragments of Ramos cell VH region DNA
CC   containing mutations other than single nucleotide substitutions. The
CC   number assigned to the mutation represents the position in the wild-type
CC   VH DNA (AAA52364) to which the first nucleotide in the mutant fragment
CC   corresponds. Sequences AAA52388-A52434 represent mutations that occur in
CC   Ramos cells which express TdT, and sequences AAA52366-A52487 represent
CC   mutations that occur in non-TdT- expressing control Ramos cells
XX
SQ   Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             36.4%;  Score 10.2;  DB 1;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 1.3e+02;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTACAG 18
              |||| | ||| ||||
Db         15 GCCCCATGTGCACAG 1


RESULT 83
AAF45958/c
ID   AAF45958 standard; DNA; 15 BP.
XX
AC   AAF45958;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #797.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 7 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             36.4%;  Score 10.2;  DB 1;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 1.3e+02;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAGTCC 25
              ||   ||||||||||
Db         15 GTTGGCAGGGAGTCC 1


RESULT 84
AAF46044/c
ID   AAF46044 standard; DNA; 15 BP.
XX
AC   AAF46044;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #883.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
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CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 2 A; 8 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             36.4%;  Score 10.2;  DB 1;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 1.3e+02;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAGTCCAG 27
              || |||||||| ||
Db         15 GTGCAGGGAGTAGAG 1


RESULT 85
AAF46043/c
ID   AAF46043 standard; DNA; 15 BP.
XX
AC   AAF46043;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #882.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 2 A; 8 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             36.4%;  Score 10.2;  DB 1;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 1.3e+02;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGTCCAGG 28
              | |||||||| |||
Db         15 TGCAGGGAGTAGAGG 1


RESULT 86
AAV50300/c
ID   AAV50300 standard; DNA; 10 BP.
XX
AC   AAV50300;
XX
DT   21-OCT-1998  (first entry)
XX
DE   Yeast tag for additional NORF chromosome 11 tag position 93528.
XX
KW   Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;
KW   eukaryotic cell; antifungal; SAGE tag; gene expression;
KW   serial analysis of gene expression; probe; ss.
XX
OS   Saccharomyces cerevisiae.
OS   Synthetic.
XX
PN   WO9832847-A2.
XX
PD   30-JUL-1998.
XX
PF   22-JAN-1998;   98WO-US001216.
XX
PR   23-JAN-1997;   97US-0035917P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1998-427943/36.
XX
PT   Yeast transcriptome - useful for modulating eukaryotic cell, for
PT   screening antifungal agents, and for identifying genes in cell cycle
PT   progression.
XX
PS   Claim 1; Page 27; 44pp; English.
XX
CC   Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene
CC   involved in cell cycle progression selected from the group of
CC   nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)
CC   tags for highly expressed genes and NORF genes are given in AAV50051 to
CC   AAV50345. The present invention describes: (1) a method of using yeast
CC   genes to modulate the cell cycle which comprises administering to a cell
CC   an isolated DNA molecule comprising a yeast gene which is involved in
CC   cell cycle progression selected from differentially expressed genes (SAGE
CC   tags given in AAV50051 to AAV50345); (2) a method for screening candidate
CC   antifungal drugs which comprises contacting a test substance with a yeast
CC   cell and monitoring expression of a yeast gene which is involved in cell
CC   cycle progression; (3) a method of identifying human genes which are
CC   involved in cell cycle progression which comprises hybridizing a probe
CC   comprising at least 10 contiguous nucleotides of a yeast gene which is
CC   differentially expressed between at least 2 phases selected from the log
CC   phase, the S phase and the G2/M phase; and (4) a probe for ascertaining
CC   the phase in the cell cycle, where the probe comprises at least 14
CC   contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to
CC   AAV50345), or as an array of probes on a solid support
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             35.7%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          14 TACAGGGAGT 23
               ||||||||||
Db          10 TACAGGGAGT 1


RESULT 87
AAF33845/c
ID   AAF33845 standard; DNA; 10 BP.
XX
AC   AAF33845;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:584.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Claim 1; Page 396; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             35.7%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          14 TACAGGGAGT 23
               ||||||||||
Db          10 TACAGGGAGT 1


RESULT 88
AAF38150/c
ID   AAF38150 standard; DNA; 10 BP.
XX
AC   AAF38150;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4889.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 174; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
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XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             35.7%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGA 21
               ||||||||||
Db          10 TGTACAGGGA 1


RESULT 89
AAF33846/c
ID   AAF33846 standard; DNA; 10 BP.
XX
AC   AAF33846;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:585.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Claim 1; Page 396; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             35.7%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          14 TACAGGGAGT 23
               ||||||||||
Db          10 TACAGGGAGT 1


RESULT 90
AAF37110/c
ID   AAF37110 standard; DNA; 10 BP.
XX
AC   AAF37110;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3849.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 137; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
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CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             35.7%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGT 23
              ||||||||||
Db         10 TACAGGGAGT 1


RESULT 91
AAF33517/c
ID   AAF33517 standard; DNA; 10 BP.
XX
AC   AAF33517;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:256.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Claim 1; Page 27; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             35.7%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGT 23
              ||||||||||
Db         10 TACAGGGAGT 1


RESULT 92
AAF33847/c
ID   AAF33847 standard; DNA; 10 BP.
XX
AC   AAF33847;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:586.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Claim 1; Page 396; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
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CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             35.7%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGT 23
              ||||||||||
Db         10 TACAGGGAGT 1


RESULT 93
AAF33850/c
ID   AAF33850 standard; DNA; 10 BP.
XX
AC   AAF33850;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:589.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Claim 1; Page 396; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             35.7%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGT 23
              ||||||||||
Db         10 TACAGGGAGT 1


RESULT 94
ABL39518
ID   ABL39518 standard; DNA; 10 BP.
XX
AC   ABL39518;
XX
DT   22-APR-2002  (first entry)
XX
DE   Human ETFB primer-extension oligonucleotide 24.
XX
KW   Human; electron-transfer flavoprotein beta polypeptide; ETFB;
KW   electron acceptor; mitochondrial matrix; glutaric acidaemia type II;
KW   novel polymorphic site; novel polymorphism; ETFB genotype; ss; GAII;
KW   ETFB haplotype; transgenic animal; primer; probe; chromosome 19q13;
KW   primer-extension oligonucleotide; single nucleotide polymorphism; SNP.
XX
OS   Homo sapiens.
XX
PN   WO200202580-A2.
XX
PD   10-JAN-2002.
XX
PF   05-JUL-2001; 2001WO-US021306.
XX
PR   05-JUL-2000; 2000US-0215984P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bentivegna SC,  Bieglecki KM,  Kazemi A,  Koshy B;
XX
DR   WPI; 2002-154722/20.
XX
PT   Novel isolated human electron-transfer-flavoprotein, beta polynucleotide,
PT   useful for therapeutic purposes, for studying the expression and function
PT   of the polynucleotide, and for expressing the flavoprotein.
XX
PS   Claim 19; Page 15; 143pp; English.
XX
CC   The invention comprises DNA, cDNA and protein sequences of the human
CC   electron-transfer flavoprotein, beta polypeptide (ETFB) gene (located on
CC   chromosome 19q13.3-13.4). The invention specifically relates to the
CC   identification of 27 novel polymorphic sites within the ETFB gene.
CC   Electron-transfer flavoprotein (ETF) is an obligatory electron acceptor
CC   for nine primary flavoprotein dehydrogenases and is located in the
CC   mitochondrial matrix. ETF is composed of an alpha (ETFA) and a beta
CC   (ETFB) subunit. Electrons accepted by ETF are transferred to the
```

```
CC   mitochondrial respiratory chain by ETF dehydrogenases (ETFDHs).
CC   Deficiency of ETF or ETFDH leads to glutaric acidaemia type II (GAII).
CC   Therefore ETFB is a pharmaceutically-important gene in the treatment of
CC   GAII. The novel ETFB polymorphisms identified in the invention are useful
CC   for genotyping and haplotyping the ETFB gene of an individual. The ETFB
CC   protein and nucleic acids of the invention are useful for studying the
CC   expression and function of ETFB in vivo. The ETFB protein and nucleic
CC   acids are also useful for testing the efficacy of therapeutic agents and
CC   compounds for glutaric acidaemia type II. The nucleic acids of the
CC   invention are useful in the production of a transgenic animal expressing
CC   the ETFB gene. Nucleic acids ABL39414-ABL39440 represent claimed ETFB
CC   allele-specific probes. Nucleic acids ABL39441-ABL39494 represent claimed
CC   ETFB allele-specific PCR primers. Nucleic acids ABL39495-ABL39548
CC   represent claimed ETFB primer-extension oligonucleotides
XX
SQ   Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             35.7%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 78;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCAGG 28
              ||||||||||
Db          1 GGAGTCCAGG 10


RESULT 95
ABQ86347/c
ID   ABQ86347 standard; cDNA; 11 BP.
XX
AC   ABQ86347;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 102.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 41; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             35.7%;  Score 10;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGA 21
              ||||||||||
Db         10 TGTACAGGGA 1


RESULT 96
ABV68461/c
ID   ABV68461 standard; cDNA; 11 BP.
XX
AC   ABV68461;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 6247.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 198; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             35.7%;  Score 10;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 91;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGA 21
              ||||||||||
Db         10 TGTACAGGGA 1


RESULT 97
AAT54219
ID   AAT54219 standard; RNA; 15 BP.
```

```
XX
AC   AAT54219;
XX
DT   25-MAR-2003  (revised)
DT   24-MAR-1997  (first entry)
XX
DE   Human IL-5 hammerhead ribozyme target sequence (nt. position 91).
XX
KW   Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW   gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW   intercellular adhesion molecule; rel A; tumour necrosis factor;
KW   TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW   translocation; chronic myelogenous leukaemia; CML; cancer;
KW   Philadelphia chromosome; inflammation; autoimmune disease;
KW   atherosclerosis; myocardial infarction; stroke; restenosis;
KW   transplant rejection; rheumatoid arthritis; psoriasis;
KW   myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW   human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO9523225-A2.
XX
PD   31-AUG-1995.
XX
PF   23-FEB-1995;   95WO-IB000156.
XX
PR   23-FEB-1994;   94US-00201109.
PR   29-MAR-1994;   94US-00218934.
PR   04-APR-1994;   94US-00222795.
PR   07-APR-1994;   94US-00224483.
PR   15-APR-1994;   94US-00227958.
PR   15-APR-1994;   94US-00228041.
PR   18-MAY-1994;   94US-00245736.
PR   06-JUL-1994;   94US-00271280.
PR   15-AUG-1994;   94US-00291932.
PR   16-AUG-1994;   94US-00291433.
PR   17-AUG-1994;   94US-00292620.
PR   19-AUG-1994;   94US-00293520.
PR   02-SEP-1994;   94US-00300000.
PR   08-SEP-1994;   94US-00303039.
PR   23-SEP-1994;   94US-00311486.
PR   23-SEP-1994;   94US-00311749.
PR   28-SEP-1994;   94US-00314397.
PR   03-OCT-1994;   94US-00316771.
PR   07-OCT-1994;   94US-00319492.
PR   11-OCT-1994;   94US-00321993.
PR   04-NOV-1994;   94US-00334847.
PR   10-NOV-1994;   94US-00337608.
PR   28-NOV-1994;   94US-00345516.
PR   16-DEC-1994;   94US-00357577.
PR   23-DEC-1994;   94US-00363233.
PR   30-JAN-1995;   95US-00380734.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Stinchcomb DT,  Chowrira B,  Direnzo A,  Draper KG,  Dudycz LW;
PI   Grimm S,  Karpeisky A,  Kisich K,  Matulic-Adamic J,  Mcswiggen JA;
PI   Modak A,  Pavco P,  Beigleman L,  Sullivan SM,  Sweedler D,  Thompson JD;
PI   Tracz D,  Usman N,  Wincott FE,  Woolf T;
XX
DR   WPI; 1995-351090/45.
XX
PT   Ribozymes having modified bases and methods for producing them - for use
PT   in inhibiting disease related genes.
XX
PS   Claim 2; Page 214; 407pp; English.
XX
CC   The present sequence represents a preferred target sequence for an
CC   enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-
CC   5) mRNA at the nucleotide base position indicated in the DE line. Regions
CC   of the mRNA that do not form secondary folding structures and that
CC   contain potential hammerhead and hairpin ribozyme cleavage sites were
CC   identified by computer analysis. Ribozymes directed against these mRNA
CC   sequences were designed and synthesised with modifications that improve
CC   their nuclease resistance. The ribozymes cleave the IL-5 target sequences
CC   and thereby inhibit IL-5 expression, making them useful for treating
CC   chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes
CC   and preventing the recruitment and activation of eosinophils. The
CC   ribozymes can also be used to treat eosinophilia (related to parasitic
CC   infection or with pulmonary infiltration) and L-tryptophan-associated
CC   eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI
CC   field.)
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;

  Query Match             35.7%;  Score 10;  DB 1;  Length 15;
  Best Local Similarity   70.0%;  Pred. No. 1.5e+02;
  Matches    7;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTA 15
              ||:|||:|:|
Db          5 CCUACGUGUA 14


RESULT 98
AAZ62686
ID   AAZ62686 standard; RNA; 15 BP.
XX
AC   AAZ62686;
XX
DT   28-MAR-2000  (first entry)
XX
DE   Substrate for HH ribozyme HCV-5596 which cleaves HCV RNA at nt. 5596.
XX
KW   Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW   cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW   autoimmune disease; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO9955847-A2.
XX
PD   04-NOV-1999.
XX
PF   26-APR-1999;   99WO-US009027.
XX
PR   27-APR-1998;   98US-0083217P.
PR   18-SEP-1998;   98US-0100842P.
PR   25-FEB-1999;   99US-00257608.
PR   23-MAR-1999;   99US-00274553.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Mcswiggen JA,  Roberts E,  Pavco PA,  Macejak D;
XX
DR   WPI; 2000-062023/05.
XX
PT   Novel ribozymes for the treatment of diseases and conditions related to
PT   hepatitis C infection.
XX
PS   Claim 1; Page 59; 123pp; English.
XX
CC   The present sequence represents the preferred target sequence of an
CC   enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC   the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC   the descriptor line. The HCV sequence was screened for optimal ribozyme
CC   target sites using a computer folding algorithm and regions of the mRNA
CC   which did not form secondary folding structures and contained potential
CC   ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC   target these sites and their activities optimised by either varying the
CC   length of the binding arms or by modification to prevent degradation by
CC   nucleases. The ribozymes of the invention inhibit gene expression and/or
CC   viral replication, and are used to treat diseases associated with
CC   Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
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CC   hepatocellular carcinoma. The ribozymes may be used in combination with
CC   interferon to treat HCV infection, other infectious diseases, autoimmune
CC   diseases, and cancer
XX
SQ   Sequence 15 BP; 2 A; 2 C; 8 G; 0 T; 3 U; 0 Other;

  Query Match             35.7%;  Score 10;  DB 1;  Length 15;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCAGG 28
              ||||:|||||
Db          3 GGAGUCCAGG 12


RESULT 99
AAF45957/c
ID   AAF45957 standard; DNA; 15 BP.
XX
AC   AAF45957;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #796.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 4 A; 6 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             35.7%;  Score 10;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCC 25
              ||||||||||
Db         11 CAGGGAGTCC 2


RESULT 100
ABL52152/c
ID   ABL52152 standard; DNA; 15 BP.
XX
AC   ABL52152;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Human PER1 allele specific oligonucleotide primer SEQ ID NO:77.
XX
KW   Human; period (Drosophila) homologue 1; PER1; polymorphic variant;
KW   polymorphic site; genotyping; haplotyping; circadian rhythm regulation;
KW   single nucleotide polymorphism; SNP; gene; primer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    14
FT                   /*tag=  a
FT                   /note= "polymorphic site indicated by an ambiguity base"
XX
PN   WO200222650-A2.
XX
PD   21-MAR-2002.
XX
PF   13-SEP-2001; 2001WO-US028780.
XX
PR   13-SEP-2000; 2000US-0232468P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Duda A,  Kliem SE,  Koshy B;
XX
DR   WPI; 2002-393941/42.
XX
PT   Novel isolated human period Drosophila homolog 1 polynucleotide, useful
PT   for therapeutic purposes, for studying the expression and function of the
PT   polynucleotide, and for expressing the homolog.
XX
PS   Claim 17; Page 15; 162pp; English.
XX
CC   The present invention describes an isolated human period (Drosophila)
CC   homologue 1, (PER1) polynucleotide (I) comprising a sequence which is a
CC   polymorphic variant for a reference sequence (ABL52077) for the PER1 gene
CC   or its fragment, or a polymorphic variant of a reference sequence
CC   (ABL52078) for a PER1 cDNA or its fragment. The present invention also
CC   describes methods for genotyping and haplotyping the PER1 gene of an
CC   individual. (I) is useful in studying the expression and function of
CC   PER1, and in expressing PER1 protein for use in screening for candidate
CC   drugs to treat diseases related to PER1 activity. (I) is useful for
CC   therapeutic purposes. A recombinant non-human organism transformed or
CC   transfected with (I) can be used for studying expression of the PER1
CC   isogenes in vivo, for in vivo screening and testing of drugs targeted
CC   against PER1 protein, and for testing the efficacy of therapeutic agents
CC   and compounds for disorders associated with circadian rhythm regulation.
CC   The present sequence represents an allele specific oligonucleotide primer
CC   for human PER1, which is used in the exemplification of the present
CC   invention
XX
SQ   Sequence 15 BP; 2 A; 7 C; 2 G; 3 T; 0 U; 1 Other;

  Query Match             35.7%;  Score 10;  DB 1;  Length 15;
```

Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          10 CGTGTACAGGGA 21
               :|||| ||||||
Db          14 YGTGTGCAGGGA 3
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RESULT 101
ABL39464
ID ABL39464 standard; DNA; 15 BP.
XX
AC ABL39464;
XX
DT 22-APR-2002 (first entry)
XX
DE Human ETFB allele-specific oligonucleotide primer 24.
XX
KW Human; electron-transfer flavoprotein beta polypeptide; ETFB;
KW electron acceptor; mitochondrial matrix; glutaric acidaemia type II;
KW novel polymorphic site; novel polymorphism; ETFB genotype; ss; GAII;
KW ETFB haplotype; transgenic animal; primer; probe; chromosome 19q13;
KW primer-extension oligonucleotide; single nucleotide polymorphism; SNP.
XX
OS Homo sapiens.
XX
PN WO200202580-A2.
XX
PD 10-JAN-2002.
XX
PF 05-JUL-2001; 2001WO-US021306.
XX
PR 05-JUL-2000; 2000US-0215984P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Bieglecki KM, Kazemi A, Koshy B;
XX
DR WPI; 2002-154722/20.
XX
PT Novel isolated human electron-transfer-flavoprotein, beta polynucleotide,
PT useful for therapeutic purposes, for studying the expression and function
PT of the polynucleotide, and for expressing the flavoprotein.
XX
PS Claim 17; Page 14; 143pp; English.
XX
CC The invention comprises DNA, cDNA and protein sequences of the human
CC electron-transfer flavoprotein, beta polypeptide (ETFB) gene (located on
CC chromosome 19q13.3-13.4). The invention specifically relates to the
CC identification of 27 novel polymorphic sites within the ETFB gene.
CC Electron-transfer flavoprotein (ETF) is an obligatory electron acceptor
CC for nine primary flavoprotein dehydrogenases and is located in the
CC mitochondrial matrix. ETF is composed of an alpha (ETFA) and a beta
CC (ETFB) subunit. Electrons accepted by ETF are transferred to the
CC mitochondrial respiratory chain by ETF dehydrogenases (ETFDHs).
CC Deficiency of ETF or ETFDH leads to glutaric acidaemia type II (GAII).
CC Therefore ETFB is a pharmaceutically-important gene in the treatment of
CC GAII. The novel ETFB polymorphisms identified in the invention are useful
CC for genotyping and haplotyping the ETFB gene of an individual. The ETFB
CC protein and nucleic acids of the invention are useful for studying the
CC expression and function of ETFB in vivo. The ETFB protein and nucleic
CC acids are also useful for testing the efficacy of therapeutic agents and
CC compounds for glutaric acidaemia type II. The nucleic acids of the
CC invention are useful in the production of a transgenic animal expressing
CC the ETFB gene. Nucleic acids ABL39414-ABL39440 represent claimed ETFB
CC allele-specific probes. Nucleic acids ABL39441-ABL39494 represent claimed
CC ETFB allele-specific PCR primers. Nucleic acids ABL39495-ABL39548
CC represent claimed ETFB primer-extension oligonucleotides
XX
SQ Sequence 15 BP; 3 A; 5 C; 5 G; 1 T; 0 U; 1 Other;

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          19 GGAGTCCAGG 28
               ||||||||||
Db           4 GGAGTCCAGG 13
```

RESULT 102
ABX00537
ID ABX00537 standard; RNA; 15 BP.
XX
AC ABX00537;
XX
DT 23-DEC-2002 (first entry)
XX
DE Hepatitis C virus substrate #319 for HCV hammerhead ribozyme #319.
XX
KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW type I interferon; interferon alpha; interferon beta; cytostatic;
KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS Hepatitis C virus.
XX
PN US2002082225-A1.
XX
PD 27-JUN-2002.
XX
PF 23-MAR-1999; 99US-00274553.
XX
PR 23-MAR-1999; 99US-00274553.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (ROBE/) ROBERTS B.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX
DR WPI; 2002-617759/66.
XX
PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT replication and are useful to treat hepatitis C virus infections and
PT cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS Claim 1; Page 30; 80pp; English.
XX
CC The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of
CC HCV. They can be used to treat cirrhosis, liver failure and/or
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC a condition associated with HCV infection in conjunction with one or more
CC other drug therapies, particularly type I interferon, especially
CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 15 BP; 2 A; 2 C; 8 G; 0 T; 3 U; 0 Other;

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          19 GGAGTCCAGG 28
               ||||:|||||
Db           3 GGAGUCCAGG 12
```

```
RESULT 103
AAV11020
ID   AAV11020 standard; RNA; 13 BP.
XX
AC   AAV11020;
XX
DT   25-MAR-2003  (revised)
DT   14-JUL-1998  (first entry)
XX
DE   Human ribozyme target sequence from HLA-DPB 02DPB #1.
XX
KW   Ribozyme; target; human lymphocyte antigen; HLA-DPB; MHC allele;
KW   major histocompatability complex; cleavage; suppression; transplant;
KW   incompatibility; autoimmune disease; juvenile diabetes;
KW   rheumatoid arthritis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9704087-A1.
XX
PD   06-FEB-1997.
XX
PF   18-JUL-1996;   96WO-EP003173.
XX
PR   18-JUL-1995;   95EP-00111256.
XX
PA   (KRUP/) KRUPP G.
PA   (MARG/) MARGET M.
PA   (WEST/) WESTPHAL E.
PA   (MUEL/) MUELLER-RUCHHOLTZ W.
XX
PI   Krupp G,  Marget M,  Westphal E,  Mueller-Ruchholtz W;
XX
DR   WPI; 1997-132628/12.
XX
PT   Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft
PT   versus host reactions, to overcome blood incompatibility and to treat
PT   auto:immune disease.
XX
PS   Claim 5; Fig 1; 76pp; German.
XX
CC   AAV10915-V11123 are target sequences for a novel ribozyme which cleaves
CC   specific alleles from the major histocompatability complex (MHC). This
CC   ribozyme contains a catalytic region and a hybridisation region which is
CC   complementary to all mRNA transcribed from vertebrate genes of a specific
CC   family of closely related MHC alleles or to mRNA from a single MHC
CC   allele, and is able to cleave such mRNA. The mRNA has a target region
CC   which in case is essentially conserved in all genes of the family but
CC   differs from genes of all other MHC alleles to such a degree that no
CC   cleavage of mRNA transcribed from these other alleles occurs. This allows
CC   the selective reduction or inhibition of expression of all genes of a
CC   family or of a single gene. This ribozyme can be used for permanent or
CC   transient suppression of expression of MHC alleles, in vivo or in vitro.
CC   Specific applications are to prevent guest vs. host or host vs. guest
CC   reactions, to prevent blood incompatibilities (partic. of the ABO, rhesus
CC   and Kell systems) and to treat autoimmune diseases such as juvenile
CC   diabetes and rheumatoid arthritis. The use of this ribozyme avoids the
CC   need for immunosuppressants in transplant patients. It provides very
CC   specific reduction of particular HLA molecules that cause incompatibility
CC   between donor and recipient. (Updated on 25-MAR-2003 to correct PA
CC   field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 13 BP; 3 A; 3 C; 4 G; 0 T; 3 U; 0 Other;
```

```
  Query Match           35.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity  61.5%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy           8 TACGTGTACAGGG 20
               :|||:|:||  ||
Db           1 UACGUGUACCAGG 13
```

```
RESULT 104
AAV11070
ID   AAV11070 standard; RNA; 13 BP.
XX
AC   AAV11070;
XX
DT   25-MAR-2003  (revised)
DT   14-JUL-1998  (first entry)
XX
DE   Human ribozyme target sequence from HLA-DQB 14DQB #1.
XX
KW   Ribozyme; target; human lymphocyte antigen; HLA-DQB; MHC allele;
KW   major histocompatability complex; cleavage; suppression; transplant;
KW   incompatibility; autoimmune disease; juvenile diabetes;
KW   rheumatoid arthritis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9704087-A1.
XX
PD   06-FEB-1997.
XX
PF   18-JUL-1996;   96WO-EP003173.
XX
PR   18-JUL-1995;   95EP-00111256.
XX
PA   (KRUP/) KRUPP G.
PA   (MARG/) MARGET M.
PA   (WEST/) WESTPHAL E.
PA   (MUEL/) MUELLER-RUCHHOLTZ W.
XX
PI   Krupp G,  Marget M,  Westphal E,  Mueller-Ruchholtz W;
XX
DR   WPI; 1997-132628/12.
XX
PT   Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft
PT   versus host reactions, to overcome blood incompatibility and to treat
PT   auto:immune disease.
XX
PS   Claim 5; Fig 1; 76pp; German.
XX
CC   AAV10915-V11123 are target sequences for a novel ribozyme which cleaves
CC   specific alleles from the major histocompatability complex (MHC). This
CC   ribozyme contains a catalytic region and a hybridisation region which is
CC   complementary to all mRNA transcribed from vertebrate genes of a specific
CC   family of closely related MHC alleles or to mRNA from a single MHC
CC   allele, and is able to cleave such mRNA. The mRNA has a target region
CC   which in case is essentially conserved in all genes of the family but
CC   differs from genes of all other MHC alleles to such a degree that no
CC   cleavage of mRNA transcribed from these other alleles occurs. This allows
CC   the selective reduction or inhibition of expression of all genes of a
CC   family or of a single gene. This ribozyme can be used for permanent or
CC   transient suppression of expression of MHC alleles, in vivo or in vitro.
CC   Specific applications are to prevent guest vs. host or host vs. guest
CC   reactions, to prevent blood incompatibilities (partic. of the ABO, rhesus
CC   and Kell systems) and to treat autoimmune diseases such as juvenile
CC   diabetes and rheumatoid arthritis. The use of this ribozyme avoids the
CC   need for immunosuppressants in transplant patients. It provides very
CC   specific reduction of particular HLA molecules that cause incompatibility
CC   between donor and recipient. (Updated on 25-MAR-2003 to correct PA
CC   field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 13 BP; 3 A; 2 C; 6 G; 0 T; 2 U; 0 Other;
```

```
  Query Match           35.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity  76.9%;  Pred. No. 1.3e+02;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy          15 ACAGGGAGTCCAG 27
               |||||| |: |||
Db           1 ACAGGGUGUGCAG 13


RESULT 105
ABF13206/c
ID   ABF13206 standard; DNA; 13 BP.
XX
AC   ABF13206;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 113203 for detecting SNP TSC0028340.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 113203; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 1 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           5 CCCTACGTGTACA 17
               ||| |||| ||||
Db          13 CCCAACGTCTACA 1


RESULT 106
ABH18793
ID   ABH18793 standard; DNA; 13 BP.
XX
AC   ABH18793;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 218770 for detecting SNP TSC0053208.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 218770; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           5 CCCTACGTGTACA 17
               |||||||| || |
Db           1 CCCTACGTTTAAA 13


RESULT 107
ABH18792/c
ID   ABH18792 standard; DNA; 13 BP.
XX
AC   ABH18792;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 218769 for detecting SNP TSC0053208.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
```

```
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 218769; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTACA 17
              ||||||||  || |
Db         13 CCCTACGTTTAAA 1


RESULT 108
ABF13210/c
ID   ABF13210 standard; DNA; 13 BP.
XX
AC   ABF13210;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 113207 for detecting SNP TSC0028340.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 113207; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTACA 17
              ||| |||| ||||
Db         13 CCCGACGTCTACA 1


RESULT 109
ABF18031
ID   ABF18031 standard; DNA; 13 BP.
XX
AC   ABF18031;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 118028 for detecting SNP TSC0029509.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 118028; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
```

```
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTACA 17
              |||||| | ||||
Db          1 CCCTACCTCTACA 13


RESULT 110
ABF04489
ID   ABF04489 standard; DNA; 13 BP.
XX
AC   ABF04489;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 104486 for detecting SNP TSC0026121.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 104486; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTACA 17
              || ||||| ||||
Db          1 CCTTACGTTTACA 13


RESULT 111
ABF13207
ID   ABF13207 standard; DNA; 13 BP.
XX
AC   ABF13207;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 113204 for detecting SNP TSC0028340.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 113204; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTACA 17
              ||| |||| ||||
Db          1 CCCAACGTCTACA 13


RESULT 112
ABF18028/c
ID   ABF18028 standard; DNA; 13 BP.
XX
AC   ABF18028;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 118025 for detecting SNP TSC0029509.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
```

```
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 118025; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTACA 17
              |||||| | ||||
Db         13 CCCTACTTCTACA 1


RESULT 113
ABF18029
ID   ABF18029 standard; DNA; 13 BP.
XX
AC   ABF18029;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 118026 for detecting SNP TSC0029509.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 118026; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTACA 17
              |||||| | ||||
Db          1 CCCTACTTCTACA 13


RESULT 114
ABH11997/c
ID   ABH11997 standard; DNA; 13 BP.
XX
AC   ABH11997;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 211974 for detecting SNP TSC0051670.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 211974; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
```

```
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 8 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAG 22
              ||||| | |||||
Db         13 CGTGTGCGGGGAG 1


RESULT 115
ABH11996
ID   ABH11996 standard; DNA; 13 BP.
XX
AC   ABH11996;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 211973 for detecting SNP TSC0051670.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 211973; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 1 A; 2 C; 8 G; 2 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAG 22
              ||||| | |||||
Db          1 CGTGTGCGGGGAG 13


RESULT 116
ABF18030/c
ID   ABF18030 standard; DNA; 13 BP.
XX
AC   ABF18030;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 118027 for detecting SNP TSC0029509.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 118027; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTACA 17
              |||||| | ||||
Db         13 CCCTACCTCTACA 1


RESULT 117
ABF04488/c
ID   ABF04488 standard; DNA; 13 BP.
XX
AC   ABF04488;
```

XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 104485 for detecting SNP TSC0026121.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 104485; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

```
  Query Match           35.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity  84.6%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTACA 17
              || ||||| ||||
Db         13 CCTTACGTTTACA 1
```

RESULT 118
ABF13211
ID ABF13211 standard; DNA; 13 BP.
XX
AC ABF13211;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 113208 for detecting SNP TSC0028340.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 113208; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

```
  Query Match           35.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity  84.6%;  Pred. No. 1.3e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTACA 17
              ||| |||| ||||
Db          1 CCCGACGTCTACA 13
```

RESULT 119
AAQ83327
ID AAQ83327 standard; DNA; 14 BP.
XX
AC AAQ83327;
XX
DT 25-MAR-2003 (revised)
DT 20-SEP-1995 (first entry)
XX
DE jub-B antisense oligonucleotide.
XX
KW c-jun; c-fos; jun-B; neuronal injury; cell death; neoplasm; antisense;
KW phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO9502051-A2.
XX
PD 19-JAN-1995.
XX
PF 06-JUL-1994; 94WO-EP002218.
XX
PR 10-JUL-1993; 93EP-00111059.
XX
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI Schlingensiepen G, Schlingensiepen R, Schlingensiepen K, Brysch W;
XX
DR WPI; 1995-066896/09.
XX
PT Use of antisense c-jun, c-fos or jun-B nucleic acids - for preventing and

```
PT   treating neuronal injury, degeneration, cell death and/or neoplasms.
XX
PS   Claim 2; Page 37; 86pp; English.
XX
CC   Antisense nucleic acid hybridising with an area of the mRNA and/or DNA
CC   comprising the genes c-jun, jun-B or c-fos, expression of which plays a
CC   causal role in neuronal injury, degeneration, cell death and/ or
CC   neoplasms, can be used to prevent and treat such conditions. c-jun
CC   antisense sequences are described in AAQ83267-321 and AAQ83440-43; jun-B
CC   antisense sequences are described in AAQ83322-63 and AAQ83444-45; and c-
CC   fos antisense sequences are described in AAQ83364-439 and AAQ83446- 51.
CC   Preferably the antisense sequences are phosphorothioate oligonucleotides
CC   since these are not destroyed as fast by endogenous factors as naturally
CC   occuring molecules. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 14 BP; 4 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 14;
  Best Local Similarity   84.6%;  Pred. No. 1.5e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          10 CGTGTACAGGGAG 22
               |||||| || |||
Db           2 CGTGTAGAGAGAG 14


RESULT 120
AAA26121
ID   AAA26121 standard; DNA; 14 BP.
XX
AC   AAA26121;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hairpin ribozyme target sequence SEQ ID NO:2619.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US008547.
XX
PR   20-APR-1998;   98US-0082404P.
PR   23-JUN-1998;   98US-00103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target sequences,
PT   used to treat cancer.
XX
PS   Claim 79; Page 98; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any catalytic
CC   nucleic acid (A') that modulates expression of the oestrogen receptor
CC   gene, are used to treat cancer (particularly of breast or endometrium),
CC   in vivo or by transforming cells ex vivo and implanting treated cells, or
CC   for other conditions associated with levels of oestrogen receptor.
CC   Because of the high selectivity for targeted RNA, (A) can also be used to
CC   correlate inhibition of gene expression with alterations in phenotype,
CC   particularly for identification of therapeutic targets, and as research
CC   reagents (for RNA, in the same way that restriction endonucleases are
CC   used with DNA). The combination of modifications in (A) improves
CC   resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC   AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC   AAA24748 to AAA25992 represent their corresponding target sequences.
CC   AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC   sequences, and AAA26107 to AAA26218 represent their corresponding target
CC   sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC   antisense oligonucleotides used in the exemplification of the present
CC   invention
XX
SQ   Sequence 14 BP; 2 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 14;
  Best Local Similarity   84.6%;  Pred. No. 1.5e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           4 GCCCTACGTGTAC 16
                ||||  |||||||
Db           2 GCCCGCCGTGTAC 14


RESULT 121
ACA60796/c
ID   ACA60796 standard; DNA; 14 BP.
XX
AC   ACA60796;
XX
DT   11-AUG-2003  (first entry)
XX
DE   DNA fragment containing SNP #3 mini-sequencing primer P1.
XX
KW   Primer; ss; multiplex genotyping; MALDI-TOF mass spectrometry;
KW   Matrix-assisted laser-desorption/ionisation time-of-flight; VSET assay;
KW   nucleotide polymorphism genotyping; sequencing.
XX
OS   Unidentified.
XX
PN   US6479242-B1.
XX
PD   12-NOV-2002.
XX
PF   27-OCT-2000; 2000US-00698505.
XX
PR   27-OCT-2000; 2000US-00698505.
XX
PA   (UYCL-) UNIV CLEVELAND STATE.
XX
PI   Guo B,  Sun X;
XX
DR   WPI; 2003-298110/29.
XX
PT   Determining a nucleotide in a nucleotide polymorphism, comprises
PT   combining the polynucleotide with a mini-sequencing primer, 3
PT   dideoxynucleotides, and a deoxynucleotide, and analyzing the products
PT   with mass spectrometry.
XX
PS   Example 4; Col 15-16; 28pp; English.
XX
CC   The invention relates to a method of determining a nucleotide in a
CC   polynucleotide, comprising combining the polynucleotide with a mini-
CC   sequencing primer, 3 dideoxynucleotides and a deoxynucleotide, and
CC   analysing the products with mass spectrometry preferably Matrix-assisted
CC   laser-desorption/ionisation time-of-flight MALDI-TOF mass spectrometry.
CC   The method is useful in genotyping a nucleotide polymorphism,
CC   particularly single nucleotide polymorphisms. The VSET assay has the
CC   advantage of having high resolution and high detection sensitivity and
CC   not requiring labelling and extensive desalting steps. The method is
CC   accurate, fast, efficient and allows for simultaneous multiplex
CC   genotyping of a number of mutation sites and is compatible with
CC   automation. The present sequence represents the DNA fragment containing
```

```
CC   single nucleotide polymorphism #3 mini-sequencing primer P1 used to
CC   illustrate the method of the invention
XX
SQ   Sequence 14 BP; 3 A; 7 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match            35.0%;  Score 9.8;  DB 1;  Length 14;
  Best Local Similarity   84.6%;  Pred. No. 1.5e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGTC 24
              ||  |||||||||
Db         14 TGGGCAGGGAGTC 2


RESULT 122
AAL60777
ID   AAL60777 standard; DNA; 14 BP.
XX
AC   AAL60777;
XX
DT   03-SEP-2003  (first entry)
XX
DE   Human HNF-1 alpha gene exon 2 specific probe #11.
XX
KW   Allele-specific primer extension; ASPE; detection; human; HNF-1alpha;
KW   hepatocyte nuclear factor-1; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003044228-A1.
XX
PD   30-MAY-2003.
XX
PF   16-NOV-2002; 2002WO-KR002143.
XX
PR   23-NOV-2001; 2001KR-00073291.
XX
PA   (SMSU ) SAMSUNG ELECTRONICS CO LTD.
XX
PI   Cho J,  Kim K,  Huh N;
XX
DR   WPI; 2003-468777/44.
XX
PT   Novel primer for use in allele-specific primer extension, has in 3'
PT   portion an allele-specific nucleotide complementary to allelic variation
PT   nucleotide of target nucleic acid and an artificial mismatch nucleotide.
XX
PS   Example 1; Page 6; 28pp; English.
XX
CC   The invention relates to an improved primer discrimination method in
CC   allele-specific primer extension (ASPE). The invention also relates to
CC   primers useful in ASPE methods, which has in 3' portion an allele-
CC   specific nucleotide complementary to allelic variation nucleotide of
CC   target nucleic acid and an artificial mismatch nucleotide. The primers
CC   are useful for increasing discrimination between primers in ASPE. The
CC   ASPE method is useful in detecting a single point mutation as well as
CC   insertion and deletion variations. The present sequence is a
CC   probe(primer) used to detect variations in human HNF-1 alpha (hepatocyte
CC   nuclear factor-1) gene exon 2. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 14 BP; 3 A; 5 C; 6 G; 0 T; 0 U; 0 Other;

  Query Match            35.0%;  Score 9.8;  DB 1;  Length 14;
  Best Local Similarity   84.6%;  Pred. No. 1.5e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAGTCCAG 27
              |||||| | ||||
Db          1 ACAGGGCGGCCAG 13


RESULT 123
AAQ26688/c
ID   AAQ26688 standard; DNA; 15 BP.
XX
AC   AAQ26688;
XX
DT   25-MAR-2003  (revised)
DT   15-JAN-1993  (first entry)
XX
DE   PDGF-B primer 1.
XX
KW   Polymerase chain reaction; PCR; c-sis; pharmaceutical compositions;
KW   wound healing; amplification; ss.
XX
OS   Homo sapiens.
XX
PN   EP495638-A2.
XX
PD   22-JUL-1992.
XX
PF   15-JAN-1992;   92EP-00300330.
XX
PR   16-JAN-1991;   91US-00641345.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Alexander DM,  Cable MB,  Dalie BL,  Narula SK;
XX
DR   WPI; 1992-243474/30.
XX
PT   Expression of mature human platelet derived growth factor-B - e.g. using
PT   plasmid pTacBiq in E. coli.
XX
PS   Disclosure; Page 13; 19pp; English.
XX
CC   The sequences given in AAQ26688-93 are primers which were used in the
CC   production of an unglycosylated, biologically active, mature human
CC   platelet derived growth factor-B (PDGF-B). The amplified sequence is
CC   identical to the sequence of c-sis. This sequence can be used for any
CC   medical condition susceptible to treatment by known PGDF's.
CC   Pharmaceutical compositions for such uses comprise an effective amount of
CC   the PDGF-B and a carrier. It can be used for wound healing and to treat
CC   skin damaged by cuts, abrasions, sun, wind, etc. (Updated on 25-MAR-2003
CC   to correct PN field.)
XX
SQ   Sequence 15 BP; 1 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match            35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 1.6e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCCAGG 28
              ||||||  |||||
Db         15 CAGGGAACCCAGG 3


RESULT 124
AAQ49379/c
ID   AAQ49379 standard; DNA; 15 BP.
XX
AC   AAQ49379;
XX
DT   25-MAR-2003  (revised)
DT   04-MAY-1994  (first entry)
XX
DE   Human PDGF-B PCR primer.
XX
KW   Platelet-derived growth factor; monomeric; binding; inhibition; stenosis;
KW   restenosis; antiproliferative; invasive cardiovascular; procedures;
KW   polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9320204-A1.
```

```
XX
PD   14-OCT-1993.
XX
PF   26-MAR-1993;   93WO-US002612.
XX
PR   30-MAR-1992;   92US-00860711.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Cable MB,  Hesson TE,  Mannarino AF;
XX
DR   WPI; 1993-336912/42.
XX
PT   Monomeric platelet-derived growth factor - useful for preventing stenosis
PT   or restenosis following invasive cardiovascular procedures.
XX
PS   Disclosure; Page 28; 41pp; English.
XX
CC   The sequence is that of a primer used in the generation by PCR of a DNA
CC   fragment encoding the mature form of monomeric human platelet- derived
CC   growth factor (PDGF-B) with lambda phage DNA (isolated from a human
CC   placental cDNA library) as template. (Updated on 25-MAR-2003 to correct
CC   PN field.)
XX
SQ   Sequence 15 BP; 1 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 1.6e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          16 CAGGGAGTCCAGG 28
               ||||||  |||||
Db          15 CAGGGAACCCAGG 3


RESULT 125
AAX09580
ID   AAX09580 standard; DNA; 15 BP.
XX
AC   AAX09580;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Human biallelic polymorphic marker upstream primer #460.
XX
KW   Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW   detection; phenotypic typing; characteristic; infection; hereditary;
KW   autoimmune disease; cancer; inflammation; drug; therapy; medicament;
KW   treatment; marker; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9820165-A2.
XX
PD   14-MAY-1998.
XX
PF   05-NOV-1997;   97WO-US020313.
XX
PR   06-NOV-1996;   96US-0030455P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Lander ES,  Wang D,  Hudson T;
XX
DR   WPI; 1998-286974/25.
XX
PT   New isolated nucleic acid segments from the human genome - used for
PT   determining polymorphic forms for use in e.g. forensics, paternity
PT   testing or phenotypic typing for disease.
XX
PS   Claim 15; Page 207; 310pp; English.
XX
CC   AAX09121-X10268 are allele-specific oligonucleotide primers used in the
CC   isolation of various biallelic polymorphic markers found in the human
CC   genome (represented in AAX10269-X12937). These primers can be used in a
CC   method for determining polymorphic forms in an individual for use in e.g.
CC   forensics, paternity testing or for phenotypic typing for diseases such
CC   as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC   dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
CC   hypercholesterolemia, polycystic kidney disease, hereditary
CC   spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC   haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC   syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC   autoimmune diseases, inflammation, cancer, diseases of the nervous
CC   system, infection by pathogenic microorganisms, and characteristics such
CC   as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC   endurance, fertility, and susceptibility or receptivity to particular
CC   drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC   segments can also be used to produce medicaments for the treatment or
CC   prophylaxis of such diseases
XX
SQ   Sequence 15 BP; 0 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 1.6e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           2 GGGCCCTACGTGT 14
               ||||||| | |||
Db           2 GGGCCCTCCCTGT 14


RESULT 126
AAZ62504
ID   AAZ62504 standard; RNA; 15 BP.
XX
AC   AAZ62504;
XX
DT   28-MAR-2000  (first entry)
XX
DE   Substrate for HH ribozyme HCV-1917 which cleaves HCV RNA at nt. 1917.
XX
KW   Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW   cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW   autoimmune disease; ss.
XX
OS   Hepatitis C virus.
XX
PN   WO9955847-A2.
XX
PD   04-NOV-1999.
XX
PF   26-APR-1999;   99WO-US009027.
XX
PR   27-APR-1998;   98US-0083217P.
PR   18-SEP-1998;   98US-0100842P.
PR   25-FEB-1999;   99US-00257608.
PR   23-MAR-1999;   99US-00274553.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Mcswiggen JA,  Roberts E,  Pavco PA,  Macejak D;
XX
DR   WPI; 2000-062023/05.
XX
PT   Novel ribozymes for the treatment of diseases and conditions related to
PT   hepatitis C infection.
XX
PS   Claim 1; Page 53; 123pp; English.
XX
CC   The present sequence represents the preferred target sequence of an
CC   enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC   the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC   the descriptor line. The HCV sequence was screened for optimal ribozyme
CC   target sites using a computer folding algorithm and regions of the mRNA
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CC   which did not form secondary folding structures and contained potential
CC   ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC   target these sites and their activities optimised by either varying the
CC   length of the binding arms or by modification to prevent degradation by
CC   nucleases. The ribozymes of the invention inhibit gene expression and/or
CC   viral replication, and are used to treat diseases associated with
CC   Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC   hepatocellular carcinoma. The ribozymes may be used in combination with
CC   interferon to treat HCV infection, other infectious diseases, autoimmune
CC   diseases, and cancer
XX
SQ   Sequence 15 BP; 4 A; 5 C; 2 G; 0 T; 4 U; 0 Other;

  Query Match           35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   61.5%;  Pred. No. 1.6e+02;
  Matches    8;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGTGTA 15
              | |||:|||: :|
Db          2 GCCCCUACGUAUA 14


RESULT 127
AAZ90850/c
ID   AAZ90850 standard; DNA; 15 BP.
XX
AC   AAZ90850;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #78.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP003351.
XX
PR   24-JUN-1998;   98JP-00214720.
PR   19-OCT-1998;   98JP-00297409.
XX
PA   (CHUS ) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders.
XX
PS   Example 1; Page 41; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family sequences
CC   were initially searched for comparison on a nucleic acid database with
CC   the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid
CC   sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59258-Z59300 and AAZ90816-
CC   Z90925 represent specific examples of probe sequences used in the search.
CC   Antibodies to the NR8 family proteins are used for the diagnosis of blood
CC   formation disorders. Compounds identified as binding to the proteins are
CC   used for the treatment of such disorders
XX
SQ   Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match           35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 1.6e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          14 TACAGGGAGTCCA 26
               | ||||||  ||||
Db          13 TCCAGGGACTCCA 1


RESULT 128
AAZ90834/c
ID   AAZ90834 standard; DNA; 15 BP.
XX
AC   AAZ90834;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #62.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP003351.
XX
PR   24-JUN-1998;   98JP-00214720.
PR   19-OCT-1998;   98JP-00297409.
XX
PA   (CHUS ) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders.
XX
PS   Example 1; Page 40; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family sequences
CC   were initially searched for comparison on a nucleic acid database with
CC   the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid
CC   sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59258-Z59300 and AAZ90816-
CC   Z90925 represent specific examples of probe sequences used in the search.
CC   Antibodies to the NR8 family proteins are used for the diagnosis of blood
CC   formation disorders. Compounds identified as binding to the proteins are
CC   used for the treatment of such disorders
XX
SQ   Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match           35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 1.6e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          14 TACAGGGAGTCCA 26
               | ||||||  ||||
Db          13 TCCAGGGACTCCA 1


RESULT 129
AAZ90885/c
ID   AAZ90885 standard; DNA; 15 BP.
XX
AC   AAZ90885;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #113.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
```

```
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP003351.
XX
PR   24-JUN-1998;   98JP-00214720.
PR   19-OCT-1998;   98JP-00297409.
XX
PA   (CHUS ) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders.
XX
PS   Example 1; Page 43; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family sequences
CC   were initially searched for comparison on a nucleic acid database with
CC   the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid
CC   sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59258-Z59300 and AAZ90816-
CC   Z90925 represent specific examples of probe sequences used in the search.
CC   Antibodies to the NR8 family proteins are used for the diagnosis of blood
CC   formation disorders. Compounds identified as binding to the proteins are
CC   used for the treatment of such disorders
XX
SQ   Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 1.6e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGTCCA 26
               | |||||| ||||
Db         13 TCCAGGGACTCCA 1


RESULT 130
AAZ90922/c
ID   AAZ90922 standard; DNA; 15 BP.
XX
AC   AAZ90922;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Human NR8 gene probe #150.
XX
KW   Haemopoietin receptor family; NR8; antibody; diagnosis;
KW   blood formation disorder; fusion protein; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO9967290-A1.
XX
PD   29-DEC-1999.
XX
PF   23-JUN-1999;   99WO-JP003351.
XX
PR   24-JUN-1998;   98JP-00214720.
PR   19-OCT-1998;   98JP-00297409.
XX
PA   (CHUS ) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI   Nomura H,  Maeda M;
XX
DR   WPI; 2000-116933/10.
XX
PT   Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT   formation disorders.
XX
PS   Example 1; Page 45; 176pp; Japanese.
XX
CC   The invention relates to the isolation of sequences encoding human
CC   haemopoietin receptor protein family NR8 genes. The NR8 family sequences
CC   were initially searched for comparison on a nucleic acid database with
CC   the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid
CC   sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59258-Z59300 and AAZ90816-
CC   Z90925 represent specific examples of probe sequences used in the search.
CC   Antibodies to the NR8 family proteins are used for the diagnosis of blood
CC   formation disorders. Compounds identified as binding to the proteins are
CC   used for the treatment of such disorders
XX
SQ   Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 1.6e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGTCCA 26
               | |||||| ||||
Db         13 TCCAGGGACTCCA 1


RESULT 131
AAC88512
ID   AAC88512 standard; RNA; 15 BP.
XX
AC   AAC88512;
XX
DT   02-MAR-2001  (first entry)
XX
DE   CREB 230 coding sequence fragment.
XX
KW   Ribozyme; retinal degradation; retinal disease; learning; memory;
KW   amylotropic lateral sclerosis; tumour suppression; ss.
XX
OS   Unidentified.
XX
PN   WO200066780-A2.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011509.
XX
PR   30-APR-1999;   99US-0131942P.
XX
PA   (UYFL ) UNIV FLORIDA.
XX
PI   Lewin AS,  Muzyczka N,  Hauswirth WW,  Teschendorf C,  Burger C;
XX
DR   WPI; 2000-687548/67.
XX
PT   Novel methods for identifying genes with selected functions comprising
PT   contacting genes with a library of ribozymes, useful for identifying
PT   genes involved in, e.g. retinal disease, learning or memory and tumor
PT   suppression.
XX
PS   Claim 16; Fig 11; 111pp; English.
XX
CC   The present invention relates to a method for identifying a gene with a
CC   selected function comprising contacting genes with a library of ribozymes
CC   and identifying at least 1 ribozyme that alters the selected function of
CC   the gene. The present sequence is a target sequence used in the present
CC   invention. The methods (and ribozymes) are useful for identifying novel
CC   genes involved in retinal degradation, retinal disease, learning or
CC   memory, amylotropic lateral sclerosis or tumour suppression, and for
CC   producing non-human animal models of diseases
XX
SQ   Sequence 15 BP; 4 A; 5 C; 4 G; 0 T; 2 U; 0 Other;
```

```
  Query Match             35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   76.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCCAGG 28
              |||  ||:|||||
Db          1 CAGACAGUCCAGG 13


RESULT 132
AAH18956
ID   AAH18956 standard; DNA; 15 BP.
XX
AC   AAH18956;
XX
DT   21-JUN-2001  (first entry)
XX
DE   UCP3 polymorphism detection allele specific primer #69.
XX
KW   UCP3; uncoupling protein 3; polymorphism; obesity; diabetes mellitus; ss.
XX
OS   Homo sapiens.
XX
PN   WO200118232-A2.
XX
PD   15-MAR-2001.
XX
PF   08-SEP-2000; 2000WO-US024784.
XX
PR   08-SEP-1999;   99US-0152789P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
PA   (STEP/) STEPHENS J C.
XX
PI   Chew A,  Choi JY,  Denton RR,  Nandabalan K;
XX
DR   WPI; 2001-218562/22.
XX
PT   Nucleic acids encoding uncoupling protein 3 (mitochondrial, proton
PT   carrier) (UCP3) proteins comprising single nucleotide polymorphisms,
PT   useful for the design of drugs for treating obesity.
XX
PS   Claim 15; Page 23; 94pp; English.
XX
CC   The present invention relates to the human uncoupling protein 3
CC   (mitochondrial, proton carrier) (UCP3) gene and polymorphisms. The
CC   polymorphisms are associated with obesity, especially diabetes mellitus
CC   associated obesity. They polymorphisms may be identified and analysed to
CC   determine whether an individual is susceptible to obesity and may be used
CC   as the basis for targeted design of drugs to treat obesity. The present
CC   sequence was used in the identification and amplification of UCP3
CC   polymorphisms
XX
SQ   Sequence 15 BP; 3 A; 3 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 1.6e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCCAGG 28
              |||||||| || |
Db          2 CAGGGAGTTCACG 14


RESULT 133
AAF45854
ID   AAF45854 standard; DNA; 15 BP.
XX
AC   AAF45854;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #693.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 38; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 3 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 1.6e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAG 22
              ||||| | |||||
Db          1 CGTGTTCCGGGAG 13


RESULT 134
AAF46041/c
ID   AAF46041 standard; DNA; 15 BP.
XX
AC   AAF46041;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #880.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
```

KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 6; Page 39; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 2 A; 8 C; 1 G; 4 T; 0 U; 0 Other;

```
  Query Match           35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity  84.6%;  Pred. No. 1.6e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCCAGG 28
              ||||||||  |||
Db         15 CAGGGAGTAGAGG 3
```

RESULT 135
AAF45852
ID AAF45852 standard; DNA; 15 BP.
XX
AC AAF45852;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGFBP2 oligonucleotide #691.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 6; Page 38; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 1 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

```
  Query Match           35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity  84.6%;  Pred. No. 1.6e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAG 22
              ||||| | |||||
Db          3 CGTGTTCCGGGAG 15
```

RESULT 136
AAF45853
ID AAF45853 standard; DNA; 15 BP.
XX
AC AAF45853;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGFBP2 oligonucleotide #692.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.

```
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 38; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 1.6e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAG 22
              ||||| | |||||
Db          2 CGTGTTCCGGGAG 14


RESULT 137
AAF46042/c
ID   AAF46042 standard; DNA; 15 BP.
XX
AC   AAF46042;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #881.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 2 A; 8 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 1.6e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCCAGG 28
              |||||||  |||
Db         14 CAGGGAGTAGAGG 2


RESULT 138
ABL52157/c
ID   ABL52157 standard; DNA; 15 BP.
XX
AC   ABL52157;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Human PER1 allele specific oligonucleotide primer SEQ ID NO:82.
XX
KW   Human; period (Drosophila) homologue 1; PER1; polymorphic variant;
KW   polymorphic site; genotyping; haplotyping; circadian rhythm regulation;
KW   single nucleotide polymorphism; SNP; gene; primer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    14
FT                   /*tag=  a
FT                   /note= "polymorphic site indicated by an ambiguity base"
XX
PN   WO200222650-A2.
XX
PD   21-MAR-2002.
XX
PF   13-SEP-2001; 2001WO-US028780.
XX
PR   13-SEP-2000; 2000US-0232468P.
```

```
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Duda A,  Kliem SE,  Koshy B;
XX
DR   WPI; 2002-393941/42.
XX
PT   Novel isolated human period Drosophila homolog 1 polynucleotide, useful
PT   for therapeutic purposes, for studying the expression and function of the
PT   polynucleotide, and for expressing the homolog.
XX
PS   Claim 17; Page 15; 162pp; English.
XX
CC   The present invention describes an isolated human period (Drosophila)
CC   homologue 1, (PER1) polynucleotide (I) comprising a sequence which is a
CC   polymorphic variant for a reference sequence (ABL52077) for the PER1 gene
CC   or its fragment, or a polymorphic variant of a reference sequence
CC   (ABL52078) for a PER1 cDNA or its fragment. The present invention also
CC   describes methods for genotyping and haplotyping the PER1 gene of an
CC   individual. (I) is useful in studying the expression and function of
CC   PER1, and in expressing PER1 protein for use in screening for candidate
CC   drugs to treat diseases related to PER1 activity. (I) is useful for
CC   therapeutic purposes. A recombinant non-human organism transformed or
CC   transfected with (I) can be used for studying expression of the PER1
CC   isogenes in vivo, for in vivo screening and testing of drugs targeted
CC   against PER1 protein, and for testing the efficacy of therapeutic agents
CC   and compounds for disorders associated with circadian rhythm regulation.
CC   The present sequence represents an allele specific oligonucleotide primer
CC   for human PER1, which is used in the exemplification of the present
CC   invention
XX
SQ   Sequence 15 BP; 0 A; 6 C; 6 G; 2 T; 0 U; 1 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 1.6e+02;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCCAGG 28
              | ||||| |||||
Db         15 CYGGGAGCCCAGG 3


RESULT 139
ABL39485/c
ID   ABL39485 standard; DNA; 15 BP.
XX
AC   ABL39485;
XX
DT   22-APR-2002  (first entry)
XX
DE   Human ETFB allele-specific oligonucleotide primer 45.
XX
KW   Human; electron-transfer flavoprotein beta polypeptide; ETFB;
KW   electron acceptor; mitochondrial matrix; glutaric acidaemia type II;
KW   novel polymorphic site; novel polymorphism; ETFB genotype; ss; GAII;
KW   ETFB haplotype; transgenic animal; primer; probe; chromosome 19q13;
KW   primer-extension oligonucleotide; single nucleotide polymorphism; SNP.
XX
OS   Homo sapiens.
XX
PN   WO200202580-A2.
XX
PD   10-JAN-2002.
XX
PF   05-JUL-2001; 2001WO-US021306.
XX
PR   05-JUL-2000; 2000US-0215984P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bentivegna SC,  Bieglecki KM,  Kazemi A,  Koshy B;
XX
DR   WPI; 2002-154722/20.
XX
PT   Novel isolated human electron-transfer-flavoprotein, beta polynucleotide,
PT   useful for therapeutic purposes, for studying the expression and function
PT   of the polynucleotide, and for expressing the flavoprotein.
XX
PS   Claim 17; Page 15; 143pp; English.
XX
CC   The invention comprises DNA, cDNA and protein sequences of the human
CC   electron-transfer flavoprotein, beta polypeptide (ETFB) gene (located on
CC   chromosome 19q13.3-13.4). The invention specifically relates to the
CC   identification of 27 novel polymorphic sites within the ETFB gene.
CC   Electron-transfer flavoprotein (ETF) is an obligatory electron acceptor
CC   for nine primary flavoprotein dehydrogenases and is located in the
CC   mitochondrial matrix. ETF is composed of an alpha (ETFA) and a beta
CC   (ETFB) subunit. Electrons accepted by ETF are transferred to the
CC   mitochondrial respiratory chain by ETF dehydrogenases (ETFDHs).
CC   Deficiency of ETF or ETFDH leads to glutaric acidaemia type II (GAII).
CC   Therefore ETFB is a pharmaceutically-important gene in the treatment of
CC   GAII. The novel ETFB polymorphisms identified in the invention are useful
CC   for genotyping and haplotyping the ETFB gene of an individual. The ETFB
CC   protein and nucleic acids of the invention are useful for studying the
CC   expression and function of ETFB in vivo. The ETFB protein and nucleic
CC   acids are also useful for testing the efficacy of therapeutic agents and
CC   compounds for glutaric acidaemia type II. The nucleic acids of the
CC   invention are useful in the production of a transgenic animal expressing
CC   the ETFB gene. Nucleic acids ABL39414-ABL39440 represent claimed ETFB
CC   allele-specific probes. Nucleic acids ABL39441-ABL39494 represent claimed
CC   ETFB allele-specific PCR primers. Nucleic acids ABL39495-ABL39548
CC   represent claimed ETFB primer-extension oligonucleotides
XX
SQ   Sequence 15 BP; 2 A; 6 C; 4 G; 2 T; 0 U; 1 Other;

  Query Match             35.0%;  Score 9.8;  DB 1;  Length 15;
  Best Local Similarity   73.3%;  Pred. No. 1.6e+02;
  Matches   11;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAGTCCAG 27
              |: |||||  |||||
Db         15 GYGCAGGGTCTCCAG 1


RESULT 140
ABA03963/c
ID   ABA03963 standard; DNA; 15 BP.
XX
AC   ABA03963;
XX
DT   19-FEB-2002  (first entry)
XX
DE   Human STK11 gene polymorphism detection ASO primer SEQ ID NO:30.
XX
KW   Human; STK11; serine/threonine kinase 11; polymorphism; SNP;
KW   single nucleotide polymorphism; Peutz-Jeghers Syndrome; genotyping;
KW   haplotype; genetic variant; haplotyping; allele-specific oligonucleotide;
KW   ASO; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200187906-A2.
XX
PD   22-NOV-2001.
XX
PF   17-MAY-2001; 2001WO-US016045.
XX
PR   17-MAY-2000; 2000US-0204697P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bieglecki KM,  Chew A,  Choi JY,  Nandabalan K,  Sausker EA;
XX
DR   WPI; 2002-055679/07.
XX
PT   Novel genetic variants of serine/threonine kinase 11 (Peutz-Jeghers
```

PT syndrome) useful in studying expression and function of the protein, and
PT for screening candidate drugs to treat diseases e.g. Peutz-Jeghers
PT syndrome.
XX
PS Claim 16; Page 13; 86pp; English.
XX
CC The present invention describes a method for haplotyping the
CC serine/threonine kinase 11 (Peutz-Jeghers syndrome) (STK11) gene of an
CC individual. STK11 gene sequences can be used in gene therapy. The STK11
CC gene is useful for screening drug targeting comprising contacting STK11
CC with a candidate agent and assaying for binding activity. STK11 is useful
CC for improving the efficiency and reliability of several steps in the
CC discovery and development of drugs for treating diseases associated with
CC STK11 activity, e.g. Peutz-Jeghers syndrome. The method is useful for
CC haplotyping the STK11 gene in an individual, which can also be used in
CC pharmaceutical research to validate STK11 as a candidate target for, and
CC in design of clinical trials of candidate drugs for, treating a specific
CC condition drugs or disease predicted to be associated with STK11
CC activity. Allele-specific oligonucleotides (ASOs) are useful as probes
CC and primers for assaying a polymorphism in the target region. The present
CC sequence represents an ASO primer used for detecting STK11 gene
CC polymorphisms, which is used in the exemplification of the present
CC invention
XX
SQ Sequence 15 BP; 2 A; 6 C; 6 G; 0 T; 0 U; 1 Other;

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGGCCCTACGTG 13
||||.|||.||||
Db 13 CGGGGCCTCCGTG 1

RESULT 141
AAD43376
ID AAD43376 standard; DNA; 15 BP.
XX
AC AAD43376;
XX
DT 14-NOV-2002 (first entry)
XX
DE Human CYP3A5 gene polymorphism detecting ASO primer #4.
XX
KW Human; cytochrome P450; subfamily IIIA; polypeptide 5 isogene; CYP3A5;
KW drug screening; polymorphism; haplotype; drug metabolising disorder;
KW gene therapy; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200246209-A2.
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US047218.
XX
PR 08-DEC-2000; 2000US-0254367P.
PR 03-MAY-2001; 2001US-0288470P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Han J, Kliem SE, Rounds E;
XX
DR WPI; 2002-636448/68.
XX
PT Novel isolated polynucleotide which is a polymorphic variant of
PT cytochrome P450, subfamily IIIA, polypeptide 5 (CYP3A5) gene useful for
PT expressing CYP3A5 protein isoform used in drug screening techniques.
XX
PS Claim 15; Page 15; 127pp; English.
XX
CC The invention relates to isolated polynucleotide having cytochrome P450,
CC subfamily IIIA, polypeptide 5 isogene (CYP3A5). The invention is useful
CC for screening drugs. The invention is useful for studying expression and
CC function of CYP3A5 and expressing CYP3A5 protein for use in screening for
CC candidate drugs to treat diseases related to CYP3A5 activity. The
CC polymorphism and haplotype data is useful for validating whether CYP3A5
CC is a suitable target for drugs to treat drug metabolising disorders,
CC screening for such drugs and reducing bias in clinical trials of such
CC drugs. The invention is also useful for therapeutic purposes. The
CC invention is useful in studying the effect of variation on the biological
CC activity of CYP3A5 as well as on the binding affinity of candidate drugs
CC to CYP3A5, or for studying the enzymatic properties of such CYP3A5
CC variants using these candidate drugs as substrate. The invention is
CC useful in gene therapy. The present sequence is human CYP3A5 gene
CC polymorphism detecting ASO (allele-specific oligonucleotide) primer
XX
SQ Sequence 15 BP; 3 A; 3 C; 7 G; 1 T; 0 U; 1 Other;

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 16 CAGGGAGTCCAGG 28
|.||||||||| |
Db 1 CGGGGAGTCCAAG 13

RESULT 142
ABK11468/c
ID ABK11468 standard; DNA; 15 BP.
XX
AC ABK11468;
XX
DT 05-JUN-2002 (first entry)
XX
DE ASO primer #4, used to detect human ADRB3 gene polymorphisms.
XX
KW Human; beta-3-adrenergic; receptor; ADRB3; primer; anorectic; ss;
KW antidiabetic; gene therapy; morbid obesity; insulin resistance;
KW non-insulin-dependent diabetes mellitus; haplotyping; SNP; ASO;
KW single nucleotide polymorphism; allele-specific oligonucleotide.
XX
OS Homo sapiens.
XX
PN WO200208425-A2.
XX
PD 31-JAN-2002.
XX
PF 23-JUL-2001; 2001WO-US023223.
XX
PR 21-JUL-2000; 2000US-0220088P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Finkel K, Koshy B;
XX
DR WPI; 2002-241571/29.
XX
PT Novel genetic variants of beta-3-adrenergic receptor gene useful in
PT studying expression and function of the protein, and for screening drugs
PT to treat diseases e.g. obesity, non-insulin dependent diabetes mellitus.
XX
PS Claim 17; Page 14; 91pp; English.
XX
CC The present invention relates to a new polypeptide comprising a sequence
CC which is a polymorphic variant of a reference sequence for ADRB3 (beta-3-
CC adrenergic receptor) protein. The reference sequence comprises a sequence
CC of 408 amino acids as given in the specification, or its fragment, and
CC the polymorphic variant comprises one or more variant amino acids. The
CC polymorphic variants are useful in studying the expression and function
CC of ADRB3, in expressing ADRB3 protein for use in screening for candidate
CC drugs to treat diseases related to ADRB3 activity, in studying the effect
CC of the variation on the biological activity of ADRB3, and the binding
CC affinity of candidate drugs targeting ADRB3 for the treatment of

CC disorders such as morbid obesity, insulin resistance and an early onset
CC of non-insulin-dependent diabetes mellitus. Haplotyping methods are
CC useful in validating ADRB3 as a candidate target for treating a specific
CC condition or disease predicted to be associated with ADRB3 activity, or
CC in the design of clinical trials of candidate drugs for treating a
CC specific condition or disease associated with ADRB3 activity. The present
CC nucleic acid sequence represents one of a collection of allele-specific
CC oligonucleotide (ASO) primers (ABK11465- ABK11488) that were used in the
CC methods of the invention to detect polymorphisms in the human ADRB3 gene
XX
SQ Sequence 15 BP; 2 A; 6 C; 4 G; 2 T; 0 U; 1 Other;

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GTGTACAGGGAGT 23
||| |||||||
Db 13 GTGCCCAGGGAGT 1

RESULT 143
ABX00355
ID ABX00355 standard; RNA; 15 BP.
XX
AC ABX00355;
XX
DT 23-DEC-2002 (first entry)
XX
DE Hepatitis C virus substrate #137 for HCV hammerhead ribozyme #137.
XX
KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW type I interferon; interferon alpha; interferon beta; cytostatic;
KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS Hepatitis C virus.
XX
PN US2002082225-A1.
XX
PD 27-JUN-2002.
XX
PF 23-MAR-1999; 99US-00274553.
XX
PR 23-MAR-1999; 99US-00274553.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (ROBE/) ROBERTS B.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX
DR WPI; 2002-617759/66.
XX
PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT replication and are useful to treat hepatitis C virus infections and
PT cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS Claim 1; Page 25; 80pp; English.
XX
CC The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of
CC HCV. They can be used to treat cirrhosis, liver failure and/or
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC a condition associated with HCV infection in conjunction with one or more
CC other drug therapies, particularly type I interferon, especially
CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 15 BP; 4 A; 5 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 1.6e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGCCCTACGTGTA 15
| |||:|||: :|
Db 2 GCCCCUACGUAUA 14

RESULT 144
ABV67167/c
ID ABV67167 standard; cDNA; 11 BP.
XX
AC ABV67167;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 4953.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 161; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 33.6%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          18 GGGAGTCCAGG 28
               |||| ||||||
Db          11 GGGATTCCAGG 1
```

RESULT 145
ABV67783/c
ID ABV67783 standard; cDNA; 11 BP.
XX
AC ABV67783;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 5569.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 179; 1345pp; German.
XX
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CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
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CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 3 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

```
  Query Match             33.6%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 1.3e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAG 22
               |||||||||  |
Db          11 TGTACAGGGTG 1
```

RESULT 146
ABV65206/c
ID ABV65206 standard; cDNA; 11 BP.
XX
AC ABV65206;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 2992.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 108; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

```
  Query Match             33.6%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 1.3e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAG 22
               |||||||| ||
Db          11 TGTACAGGAAG 1
```

RESULT 147
ABV67685/c
ID ABV67685 standard; cDNA; 11 BP.
XX
AC ABV67685;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 5471.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX

```
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 176; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 1.3e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          18 GGGAGTCCAGG 28
               |||||| ||||
Db          11 GGGAGTACAGG 1


RESULT 148
ABI40444
ID   ABI40444 standard; DNA; 12 BP.
XX
AC   ABI40444;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 340417 for detecting SNP TSC0041516.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 340417; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 1.5e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           5 CCCTACGTGTA 15
               |||||||| ||
Db           1 CCCTACGTTTA 11


RESULT 149
ABH89502/c
ID   ABH89502 standard; DNA; 12 BP.
XX
AC   ABH89502;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 289495 for detecting SNP TSC0013961.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 289495; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
```

```
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 1.5e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAGT 23
              ||| |||||||
Db         12 GTATAGGGAGT 2


RESULT 150
ABI54047/c
ID   ABI54047 standard; DNA; 12 BP.
XX
AC   ABI54047;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 354020 for detecting SNP TSC0048852.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 354020; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 1.5e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAG 22
              |||| ||||||
Db         11 TGTAGAGGGAG 1


RESULT 151
ABI23376/c
ID   ABI23376 standard; DNA; 12 BP.
XX
AC   ABI23376;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 323349 for detecting SNP TSC0031342.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 323349; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 1.5e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTA 15
              ||||||| |||
Db         11 CCCTACGCGTA 1


RESULT 152
ABI21821/c
ID   ABI21821 standard; DNA; 12 BP.
XX
AC   ABI21821;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 321794 for detecting SNP TSC0030495.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
```

```
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 321794; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 1.5e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAG 22
               |||| ||||||
Db          11 TGTATAGGGAG 1


RESULT 153
ABF19283
ID   ABF19283 standard; DNA; 13 BP.
XX
AC   ABF19283;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 119280 for detecting SNP TSC0029787.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 119280; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
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CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 3 C; 1 G; 4 T; 0 U; 1 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           7 CTACGTGTACA 17
               |||||| ||||
Db           3 CTACGTTTACA 13


RESULT 154
ABC62107
ID   ABC62107 standard; DNA; 13 BP.
XX
AC   ABC62107;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 62124 for detecting SNP TSC0016499.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 62124; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
```

```
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTA 15
              |||||||| ||
Db          2 CCCTACGTATA 12


RESULT 155
ABF44695
ID   ABF44695 standard; DNA; 13 BP.
XX
AC   ABF44695;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 144692 for detecting SNP TSC0036396.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 144692; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 1 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              |||||| ||||
Db          3 CTACGTCTACA 13


RESULT 156
ABC69525
ID   ABC69525 standard; DNA; 13 BP.
XX
AC   ABC69525;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 69542 for detecting SNP TSC0018095.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 69542; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTA 15
              |||||||| ||
Db          1 CCCTACGTCTA 11


RESULT 157
ABC54450/c
ID   ABC54450 standard; DNA; 13 BP.
XX
```

```
AC   ABC54450;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 54467 for detecting SNP TSC0014930.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 54467; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 1 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   76.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTAC 16
              :||||||||  | |
Db         13 RCCCTACGTATTC 1


RESULT 158
ABF19282/c
ID   ABF19282 standard; DNA; 13 BP.
XX
AC   ABF19282;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 119279 for detecting SNP TSC0029787.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 119279; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 1 C; 3 G; 4 T; 0 U; 1 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              |||||| ||||
Db         11 CTACGTTTACA 1


RESULT 159
ABF44694/c
ID   ABF44694 standard; DNA; 13 BP.
XX
AC   ABF44694;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 144691 for detecting SNP TSC0036396.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
```

```
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 144691; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 1 Other;

  Query Match            33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity  90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACA 17
              |||||| ||||
Db         11 CTACGTCTACA 1


RESULT 160
ABH01278/c
ID   ABH01278 standard; DNA; 13 BP.
XX
AC   ABH01278;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 201255 for detecting SNP TSC0049513.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 201255; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match            33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity  90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTAC 16
              ||||||| |||
Db         11 CCTACGTATAC 1


RESULT 161
ABF63816/c
ID   ABF63816 standard; DNA; 13 BP.
XX
AC   ABF63816;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 163813 for detecting SNP TSC0041149.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 163813; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match            33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity  90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTAC 16
```

```
                  ||||||| |||
Db          12 CCTACGTCTAC 2


RESULT 162
ABC18273/c
ID   ABC18273 standard; DNA; 13 BP.
XX
AC   ABC18273;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 18280 for detecting SNP TSC0003884.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 18280; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 6 A; 3 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAG 18
              |||||||| ||
Db         11 TACGTGTATAG 1


RESULT 163
ABF25737/c
ID   ABF25737 standard; DNA; 13 BP.
XX
AC   ABF25737;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 125734 for detecting SNP TSC0031438.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 125734; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 1 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   76.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAGTC 24
               ||||  ||||||:
Db          13 TGTATTGGGAGTY 1


RESULT 164
ABF71706
ID   ABF71706 standard; DNA; 13 BP.
XX
AC   ABF71706;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 171703 for detecting SNP TSC0042797.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
```

PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 171703; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 1 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 33.6%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 18 GGGAGTCCAGG 28
||||||| |||
Db 2 GGGAGTCGAGG 12

RESULT 165
ABH47552
ID ABH47552 standard; DNA; 13 BP.
XX
AC ABH47552;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 247529 for detecting SNP TSC0060486.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 247529; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 1 Other;

Query Match 33.6%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.6e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 12 TGTACAGGGAGTC 24
||| |||||||:
Db 1 TGTGTAGGGAGTY 13

RESULT 166
ABC54451
ID ABC54451 standard; DNA; 13 BP.
XX
AC ABC54451;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 54468 for detecting SNP TSC0014930.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 54468; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

```
XX
SQ   Sequence 13 BP; 2 A; 5 C; 1 G; 4 T; 0 U; 1 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   76.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTAC 16
              :||||||||| | |
Db          1 RCCCTACGTATTC 13


RESULT 167
ABH42658/c
ID   ABH42658 standard; DNA; 13 BP.
XX
AC   ABH42658;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 242635 for detecting SNP TSC0059191.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 242635; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 1 C; 4 G; 3 T; 0 U; 1 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTAC 16
              ||||||| |||
Db         12 CCTACGTATAC 2


RESULT 168
ABH07266
ID   ABH07266 standard; DNA; 13 BP.
XX
AC   ABH07266;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 207243 for detecting SNP TSC0007000.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 207243; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 1 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   76.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGTC 24
              ||||  ||||||:
Db          1 TGTAGGGGGAGTY 13


RESULT 169
ABH42837
ID   ABH42837 standard; DNA; 13 BP.
XX
AC   ABH42837;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 242814 for detecting SNP TSC0059260.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
```

```
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 242814; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 1 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   76.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTAC 16
              :|||||| | |||
Db          1 RCCCTACTTATAC 13


RESULT 170
ABC51399/c
ID   ABC51399 standard; DNA; 13 BP.
XX
AC   ABC51399;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 51416 for detecting SNP TSC0014352.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 51416; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          13 GTACAGGGAGT 23
               ||| |||||||
Db          12 GTATAGGGAGT 2


RESULT 171
ABH47553/c
ID   ABH47553 standard; DNA; 13 BP.
XX
AC   ABH47553;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 247530 for detecting SNP TSC0060486.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 247530; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
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```
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 1 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   76.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGTC 24
              |||  |||||||:
Db         13 TGTGTAGGGAGTY 1


RESULT 172
ABF63817
ID   ABF63817 standard; DNA; 13 BP.
XX
AC   ABF63817;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 163814 for detecting SNP TSC0041149.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 163814; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTAC 16
              ||||||| |||
Db          2 CCTACGTCTAC 12


RESULT 173
ABH42836/c
ID   ABH42836 standard; DNA; 13 BP.
XX
AC   ABH42836;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 242813 for detecting SNP TSC0059260.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 242813; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 1 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   76.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTGTAC 16
              :|||||| | |||
Db         13 RCCCTACTTATAC 1


RESULT 174
ABH01279
ID   ABH01279 standard; DNA; 13 BP.
XX
AC   ABH01279;
XX
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```
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 201256 for detecting SNP TSC0049513.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 201256; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTAC 16
              ||||||| |||
Db          3 CCTACGTATAC 13


RESULT 175
ABH07267/c
ID   ABH07267 standard; DNA; 13 BP.
XX
AC   ABH07267;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 207244 for detecting SNP TSC0007000.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 207244; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 1 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   76.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAGTC 24
               |||| ||||||:
Db          13 TGTAGGGGGAGTY 1


RESULT 176
ABH42659
ID   ABH42659 standard; DNA; 13 BP.
XX
AC   ABH42659;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 242636 for detecting SNP TSC0059191.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
```

```
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 242636; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 4 C; 1 G; 4 T; 0 U; 1 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTAC 16
              ||||||| |||
Db          2 CCTACGTATAC 12


RESULT 177
ABC51398
ID   ABC51398 standard; DNA; 13 BP.
XX
AC   ABC51398;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 51415 for detecting SNP TSC0014352.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 51415; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAGT 23
              ||| |||||||
Db          2 GTATAGGGAGT 12


RESULT 178
ABC18272
ID   ABC18272 standard; DNA; 13 BP.
XX
AC   ABC18272;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 18279 for detecting SNP TSC0003884.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 18279; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 1 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAG 18
              |||||||| ||
Db          3 TACGTGTATAG 13
```

```
RESULT 179
ABC62106/c
ID   ABC62106 standard; DNA; 13 BP.
XX
AC   ABC62106;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 62123 for detecting SNP TSC0016499.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 62123; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTA 15
              ||||||| ||
Db         12 CCCTACGTATA 2


RESULT 180
ABC69524/c
ID   ABC69524 standard; DNA; 13 BP.
XX
AC   ABC69524;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 69541 for detecting SNP TSC0018095.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 69541; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 1 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTA 15
              ||||||| ||
Db         13 CCCTACGTCTA 3


RESULT 181
ABF25736
ID   ABF25736 standard; DNA; 13 BP.
XX
AC   ABF25736;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 125733 for detecting SNP TSC0031438.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
```

```
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 125733; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 1 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   76.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGTC 24
              ||||  ||||||:
Db          1 TGTATTGGGAGTY 13


RESULT 182
ABF71707/c
ID   ABF71707 standard; DNA; 13 BP.
XX
AC   ABF71707;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 171704 for detecting SNP TSC0042797.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 171704; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 1 A; 8 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 1.6e+02;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAGG 28
              ||||||| |||
Db         12 GGGAGTCGAGG 2


RESULT 183
AAV92058
ID   AAV92058 standard; RNA; 14 BP.
XX
AC   AAV92058;
XX
DT   18-FEB-1999  (first entry)
XX
DE   Human C-raf target sequence nucleotide position 2431.
XX
KW   Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW   target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW   screening; identification; synthesis; deprotection; purification; cancer;
KW   inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
KW   restenosis; rheumatoid arthritis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9850530-A2.
XX
PD   12-NOV-1998.
XX
PF   05-MAY-1998;   98WO-US009249.
XX
PR   09-MAY-1997;   97US-0046059P.
PR   09-JUN-1997;   97US-0049002P.
PR   03-JUL-1997;   97US-0051718P.
PR   22-AUG-1997;   97US-0056808P.
PR   02-OCT-1997;   97US-0061321P.
PR   02-OCT-1997;   97US-0061324P.
PR   05-NOV-1997;   97US-0064866P.
PR   19-DEC-1997;   97US-0068212P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Jarvis T,  Matulic-Adamic J,  Reynolds M,  Kisich K,  Bellon L;
PI   Parry T,  Beigelman L,  Mcswiggen JA,  Karpeisky A,  Burgin A;
PI   Thompson J,  Workman CT,  Beaudry A,  Sweedler D;
XX
DR   WPI; 1999-009494/01.
XX
PT   Identifying new catalytic nucleic acid that modulates selected processes
PT   - especially ribozymes that cleave Raf RNA for treating cancer,
PT   restenosis, and also new ribozymes and modified nucleoside triphosphates
PT   used as antiviral agents and synthons.
XX
PS   Claim 179; Page 156; 259pp; English.
XX
CC   A method has been developed for the identification of a nucleic acid
CC   capable of modulating a process in a biological system. The method
```

```
CC   comprises: (a) introducing into the system a random library of nucleic
CC   acid catalysts (NAC) having a substrate binding domain (SBD), comprising
CC   a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC   in systems where modulation has occurred and/or determining the sequence
CC   of at least part of the SBDs in such systems. Nucleic acid molecules with
CC   endonuclease activity and catalytic activity, from the present invention,
CC   are used to modulate gene expression in plant and mammalian cells and to
CC   cleave target nucleic acid, particularly for treating systemic diseases
CC   caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
CC   ascites and infection. They may also be used to detect genetic drift and
CC   mutations in diseased cells and to determine c-raf RNA. Specifically NACs
CC   with RNA-cleaving activity that modulate expression of the Raf gene, are
CC   used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
CC   generally any condition associated with the level of c-raf. Introduction
CC   of sugar/phosphate modifications increases stability against nuclease and
CC   activity. AAV90922 to AAV93877 represent NACs that can be used in the
CC   method, specifically for modulating the expression of a Raf gene
XX
SQ   Sequence 14 BP; 3 A; 6 C; 4 G; 0 T; 1 U; 0 Other;

  Query Match             33.6%;  Score 9.4;  DB 1;  Length 14;
  Best Local Similarity   81.8%;  Pred. No. 1.8e+02;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTCCAG 27
               ||| ||:||||
Db          1 AGGCAGUCCAG 11


RESULT 184
AAQ52942/c
ID   AAQ52942 standard; RNA; 14 BP.
XX
AC   AAQ52942;
XX
DT   25-MAR-2003  (revised)
DT   26-MAY-1994  (first entry)
XX
DE   Herpes simplex virus target sequence 20.
XX
KW   RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; HnRNA;
KW   picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;
KW   papilloma virus; HPV; Epstein-Barr virus; EBV; TCLV;
KW   T-cell leukaemia virus; hepatitis C virus; HCV; cytomegalovirus;
KW   influenza virus; HSV; herpes simplex virus; vector; immune response;
KW   antibody; ribozyme; viral RNA; treatment; ss.
XX
OS   Synthetic.
XX
PN   WO9323569-A1.
XX
PD   25-NOV-1993.
XX
PF   29-APR-1993;   93WO-US004020.
XX
PR   11-MAY-1992;   92US-00882689.
PR   14-MAY-1992;   92US-00882712.
PR   14-MAY-1992;   92US-00882713.
PR   14-MAY-1992;   92US-00882714.
PR   14-MAY-1992;   92US-00882823.
PR   14-MAY-1992;   92US-00882824.
PR   14-MAY-1992;   92US-00882886.
PR   14-MAY-1992;   92US-00882888.
PR   14-MAY-1992;   92US-00882889.
PR   14-MAY-1992;   92US-00882921.
PR   14-MAY-1992;   92US-00882922.
PR   14-MAY-1992;   92US-00883823.
PR   14-MAY-1992;   92US-00883849.
PR   14-MAY-1992;   92US-00884073.
PR   14-MAY-1992;   92US-00884074.
PR   14-MAY-1992;   92US-00884333.
PR   14-MAY-1992;   92US-00884422.
PR   14-MAY-1992;   92US-00884431.
PR   14-MAY-1992;   92US-00884436.
PR   14-MAY-1992;   92US-00884521.
PR   31-JUL-1992;   92US-00923738.
PR   26-AUG-1992;   92US-00935854.
PR   26-AUG-1992;   92US-00936086.
PR   18-SEP-1992;   92US-00948359.
PR   15-OCT-1992;   92US-00963322.
PR   07-DEC-1992;   92US-00987129.
PR   07-DEC-1992;   92US-00987130.
PR   07-DEC-1992;   92US-00987133.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Draper KG,  Dudycz LW,  Mcswiggen JA,  Macejak DG,  Holecek JJ;
PI   Mamone JA;
XX
DR   WPI; 1993-386599/48.
XX
PT   Enzymatic RNA molecules - used to inhibit viral replication, infection
PT   and gene expression.
XX
PS   Claim 5; Fig 15; 287pp; English.
XX
CC   The sequences (AAQ52923-Q53037) are pref. herpes simplex virus target
CC   sequences for enzymatic RNA molecules. The RNA molecules are
CC   complementary to a substrate binding region in the specified gene target.
CC   They also have enzymatic activity, in that they specifically cleave RNA
CC   in the target. The ERMs interfere with viral replication and therefore
CC   have anti-viral properties. They can be used to attenuate viruses to be
CC   used in vaccines. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC   on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct
CC   PI field.)
XX
SQ   Sequence 14 BP; 3 A; 6 C; 3 G; 0 T; 2 U; 0 Other;

  Query Match             32.9%;  Score 9.2;  DB 1;  Length 14;
  Best Local Similarity   78.6%;  Pred. No. 2e+02;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAGT 23
              ||||  ||||| ||
Db         14 CGTGATCAGGGCGT 1


RESULT 185
AAQ83430/c
ID   AAQ83430 standard; DNA; 14 BP.
XX
AC   AAQ83430;
XX
DT   25-MAR-2003  (revised)
DT   20-SEP-1995  (first entry)
XX
DE   c-fos antisense oligonucleotide.
XX
KW   c-jun; c-fos; jun-B; neuronal injury; cell death; neoplasm; antisense;
KW   phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO9502051-A2.
XX
PD   19-JAN-1995.
XX
PF   06-JUL-1994;   94WO-EP002218.
XX
PR   10-JUL-1993;   93EP-00111059.
XX
PA   (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI   Schlingensiepen G,  Schlingensiepen R,  Schlingensiepen K,  Brysch W;
XX
DR   WPI; 1995-066896/09.
```

```
XX
PT   Use of antisense c-jun, c-fos or jun-B nucleic acids - for preventing and
PT   treating neuronal injury, degeneration, cell death and/or neoplasms.
XX
PS   Claim 2; Page 65; 86pp; English.
XX
CC   Antisense nucleic acid hybridising with an area of the mRNA and/or DNA
CC   comprising the genes c-jun, jun-B or c-fos, expression of which plays a
CC   causal role in neuronal injury, degeneration, cell death and/ or
CC   neoplasms, can be used to prevent and treat such conditions. c-jun
CC   antisense sequences are described in AAQ83267-321 and AAQ83440-43; jun-B
CC   antisense sequences are described in AAQ83322-63 and AAQ83444-45; and c-
CC   fos antisense sequences are described in AAQ83364-439 and AAQ83446- 51.
CC   Preferably the antisense sequences are phosphorothioate oligonucleotides
CC   since these are not destroyed as fast by endogenous factors as naturally
CC   occuring molecules. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 14 BP; 4 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             32.9%;  Score 9.2;  DB 1;  Length 14;
  Best Local Similarity   78.6%;  Pred. No. 2e+02;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACAGG 19
              |||  || ||||||
Db         14 CCTCTGTATACAGG 1


RESULT 186
AAA98696
ID   AAA98696 standard; DNA; 10 BP.
XX
AC   AAA98696;
XX
DT   07-FEB-2001  (first entry)
XX
DE   Nucleic acid combinatorial primer DNA #1.
XX
KW   Nucleic acid combination; hybridization; identification; gene chip;
KW   DNA fingerprinting; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200056921-A2.
XX
PD   28-SEP-2000.
XX
PF   21-MAR-2000; 2000WO-EP002492.
XX
PR   22-MAR-1999;   99DE-01012983.
PR   24-SEP-1999;   99DE-01045765.
XX
PA   (CULL/) CULLEN P.
PA   (SEED/) SEEDORF U.
PA   (LORK/) LORKOWSKI S.
XX
PI   Cullen P,  Seedorf U,  Lorkowski S;
XX
DR   WPI; 2000-628273/60.
XX
PT   Nucleic acid combination, useful for hybridization, e.g. genomic,
PT   analysis, comprises a combinatorial oligomer linked to a specific
PT   complementary sequence.
XX
PS   Example 1; Page 9; 19pp; German.
XX
CC   This invention describes a novel nucleic acid combination (A) comprising
CC   an n-mer (I) and at least one sequence (II) complementary to a reference
CC   sequence (III). The invention also describes a process comprising
CC   hybridization of a nucleic acid with a combination of (II) complementary
CC   to at least one (III). (A) are used for identifying nucleic acids by
CC   hybridization, e.g. for genomic analysis; examination of gene expression
CC   and DNA fingerprinting. Elongation of (I) by (II) stabilizes base
CC   pairing. Since all (A) include the same (II), the number of potential
CC   combinations of a selected n-mer does not increase, in spite of the
CC   increase in sequence specificity, so that difficulties associated with
CC   the limited amount of space available on a gene chip are avoided. (A)
CC   binds only to target sequences complementary to both (I) and (II),
CC   significantly reducing the number of actual target sequences (compared
CC   with the 500-5000 mRNAs that are potential binding partners for any given
CC   nonamer), i.e. the gene specificity is increased, even for short n-mers
XX
SQ   Sequence 10 BP; 2 A; 2 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             32.1%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              |||||||||
Db          1 TACGTGTAC 9


RESULT 187
AAA56564
ID   AAA56564 standard; DNA; 10 BP.
XX
AC   AAA56564;
XX
DT   07-SEP-2000  (first entry)
XX
DE   Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:458.
XX
KW   Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
KW   granulocyte-macrophage colony-stimulating factor; characterisation;
KW   GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
KW   disease onset mechanism; genetic disease; drug development; ss.
XX
OS   Homo sapiens.
XX
PN   WO200024892-A1.
XX
PD   04-MAY-2000.
XX
PF   28-OCT-1999;   99WO-JP005982.
XX
PR   28-OCT-1998;   98JP-00307532.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Hashimoto S,  Matsushima K,  Suzuki T;
XX
DR   WPI; 2000-350734/30.
XX
PT   Genes most frequently expressed in human monocytes and GM-macrophages and
PT   M-macrophages studied and with cDNAs characterized, for study of gene
PT   specificity, disease onset mechanism, drug development and diagnosis.
XX
PS   Claim 49; Page 130; 138pp; Japanese.
XX
CC   The present invention describes 100 human genes, which are expressed most
CC   frequently in human monocytes. The cDNA of each gene has a sequence fully
CC   defined in the specification, and lacking the CATG sequence located
CC   adjacent to polyA region. Also described are: (1) an antibody
CC   specifically for the protein encoded by any of the genes; (2)
CC   oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
CC   which are expressed most frequently in human macrophages, differentiated
CC   from human monocytes by granulocyte-macrophage colony-stimulating factor,
CC   the cDNA of each gene has a fully defined sequence, given in the
CC   specification, lacking the base sequence CATG located most closely to the
CC   poly A region; (4) an antibody specifically for the protein encoded by
CC   any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
CC   sequences of (3). The genes and cDNAs, are used for the study of gene
CC   specificity and disease onset mechanism e.g. oncogenesis, genetic
CC   diseases, drug development and diagnosis. AAA56107 to AAA56586 represent
CC   specifically claimed oligonucleotide tag sequences for human genes
```

```
CC   expressed in monocytes and macrophages
XX
SQ   Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match            32.1%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 1.4e+02;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTCC 25
              |||||||||
Db          2 AGGGAGTCC 10


RESULT 188
AAH63189
ID   AAH63189 standard; cDNA; 10 BP.
XX
AC   AAH63189;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human colon epithelium specific transcriptome sequence SEQ ID NO: 29.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US031922.
XX
PR   24-NOV-1999;   99US-00448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell type,
PT   such as cancer cell, comprises transcriptomes expressed in particular
PT   cell types.
XX
PS   Claim 1; Page 39; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences AAH63161-
CC   AAH64724 is expressed by the cell. The transcriptomes described in the
CC   invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of the
CC   transcriptomes described in the exemplification of the invention
XX
SQ   Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match            32.1%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 1.4e+02;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GAGTCCAGG 28
              |||||||||
Db          2 GAGTCCAGG 10


RESULT 189
AAH20567/c
ID   AAH20567 standard; DNA; 10 BP.
XX
AC   AAH20567;
XX
DT   09-AUG-2001  (first entry)
XX
DE   Human MTR1 intron10/exon11 junction.
XX
KW   MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;
KW   transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;
KW   11p15.5 abnormality; chromosome 11; anticancer; developmental activity;
KW   intracellular calcium ion regulation; hormone; growth factor; apoptosis;
KW   cell growth; cell death; cell differentiation; urogenital disease;
KW   polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
KW   rhabdomyosarcoma; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   intron          1. .5
FT                   /*tag=  a
FT                   /number= 10
FT   exon            6. .10
FT                   /*tag=  b
FT                   /number= 11
XX
PN   WO200132693-A2.
XX
PD   10-MAY-2001.
XX
PF   06-NOV-2000; 2000WO-DE003876.
XX
PR   04-NOV-1999;   99DE-01053167.
XX
PA   (UYGU-) UNIV GUTENBERG JOHANNES.
XX
PI   Prawitt D,  Pelletier J,  Zabel B;
XX
DR   WPI; 2001-316417/33.
XX
PT   DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann
PT   syndrome and tumors, also related proteins and antibodies.
XX
PS   Example 2; Fig 2; 46pp; German.
XX
CC   This invention describes a novel DNA sequence (I) encoding the MTR1
CC   protein that: (i) has at least one biological activity of a TRP
CC   (transient receptor potential) family protein; (ii) is connected with
CC   etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected
CC   with tumors involving 11p15.5 abnormalities. The products of the
CC   invention have anticancer and developmental activity. MRT1 is involved in
CC   regulation of intracellular calcium ion levels, which are essential for
CC   cellular responses to hormones and/or growth factors; also in apoptosis
CC   and cell growth, death and differentiation, and in urogenital diseases,
CC   including polycystic kidney disease. (I) and related ribozymes, antisense
CC   RNA, proteins and antibodies (Ab)) are used to treat or prevent diseases
CC   associated with altered expression of the MRT1 gene or activity of its
CC   protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,
CC   rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also
CC   used for diagnosis of such diseases. (I) can also be used for recombinant
CC   production of MRT1 proteins (II) (used for analysis, characterization and
CC   therapy), as tissue or chromosomal markers, for identifying genetic
CC   diseases and related sequences, as primers for genetic fingerprinting, as
CC   source of oligonucleotides for biochips, and to raise anti-protein or
CC   anti-DNA antibodies. (II) are used to raise Ab, as reagents in
CC   competitive assays for (II), as tissue markers; for identifying
CC   interacting proteins and in screening for (ant)agonists. This sequence
CC   represents human MTR1 gene intron10/exon11 junction region described in
CC   the method of the invention
XX
SQ   Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match            32.1%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 1.4e+02;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          3 GGCCCTACG 11
              |||||||||
Db          9 GGCCCTACG 1


RESULT 190
AAF37219
ID   AAF37219 standard; DNA; 10 BP.
XX
AC   AAF37219;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3958.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 141; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match           32.1%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              |||||||||
Db          2 TACGTGTAC 10


RESULT 191
AAF40677
ID   AAF40677 standard; DNA; 10 BP.
XX
AC   AAF40677;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7416.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 264; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
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```
SQ   Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             32.1%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTC 24
              |||||||||
Db          1 CAGGGAGTC 9


RESULT 192
ABL39519/c
ID   ABL39519 standard; DNA; 10 BP.
XX
AC   ABL39519;
XX
DT   22-APR-2002  (first entry)
XX
DE   Human ETFB primer-extension oligonucleotide 25.
XX
KW   Human; electron-transfer flavoprotein beta polypeptide; ETFB;
KW   electron acceptor; mitochondrial matrix; glutaric acidaemia type II;
KW   novel polymorphic site; novel polymorphism; ETFB genotype; ss; GAII;
KW   ETFB haplotype; transgenic animal; primer; probe; chromosome 19q13;
KW   primer-extension oligonucleotide; single nucleotide polymorphism; SNP.
XX
OS   Homo sapiens.
XX
PN   WO200202580-A2.
XX
PD   10-JAN-2002.
XX
PF   05-JUL-2001; 2001WO-US021306.
XX
PR   05-JUL-2000; 2000US-0215984P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bentivegna SC,  Bieglecki KM,  Kazemi A,  Koshy B;
XX
DR   WPI; 2002-154722/20.
XX
PT   Novel isolated human electron-transfer-flavoprotein, beta polynucleotide,
PT   useful for therapeutic purposes, for studying the expression and function
PT   of the polynucleotide, and for expressing the flavoprotein.
XX
PS   Claim 19; Page 15; 143pp; English.
XX
CC   The invention comprises DNA, cDNA and protein sequences of the human
CC   electron-transfer flavoprotein, beta polypeptide (ETFB) gene (located on
CC   chromosome 19q13.3-13.4). The invention specifically relates to the
CC   identification of 27 novel polymorphic sites within the ETFB gene.
CC   Electron-transfer flavoprotein (ETF) is an obligatory electron acceptor
CC   for nine primary flavoprotein dehydrogenases and is located in the
CC   mitochondrial matrix. ETF is composed of an alpha (ETFA) and a beta
CC   (ETFB) subunit. Electrons accepted by ETF are transferred to the
CC   mitochondrial respiratory chain by ETF dehydrogenases (ETFDHs).
CC   Deficiency of ETF or ETFDH leads to glutaric acidaemia type II (GAII).
CC   Therefore ETFB is a pharmaceutically-important gene in the treatment of
CC   GAII. The novel ETFB polymorphisms identified in the invention are useful
CC   for genotyping and haplotyping the ETFB gene of an individual. The ETFB
CC   protein and nucleic acids of the invention are useful for studying the
CC   expression and function of ETFB in vivo. The ETFB protein and nucleic
CC   acids are also useful for testing the efficacy of therapeutic agents and
CC   compounds for glutaric acidaemia type II. The nucleic acids of the
CC   invention are useful in the production of a transgenic animal expressing
CC   the ETFB gene. Nucleic acids ABL39414-ABL39440 represent claimed ETFB
CC   allele-specific probes. Nucleic acids ABL39441-ABL39494 represent claimed
CC   ETFB allele-specific PCR primers. Nucleic acids ABL39495-ABL39548
CC   represent claimed ETFB primer-extension oligonucleotides
XX
SQ   Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             32.1%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GAGTCCAGG 28
              |||||||||
Db         10 GAGTCCAGG 2


RESULT 193
ABV67716/c
ID   ABV67716 standard; cDNA; 11 BP.
XX
AC   ABV67716;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 5502.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 177; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             32.1%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              |||||||||
Db         11 TACGTGTAC 3


RESULT 194
ABV65836/c
ID   ABV65836 standard; cDNA; 11 BP.
```

XX
AC ABV65836;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 3622.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 125; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 5 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 32.1%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GGAGTCCAG 27
||||||||| |
Db 9 GGAGTCCAG 1

RESULT 195
AAT11911/c
ID AAT11911 standard; DNA; 12 BP.
XX
AC AAT11911;
XX
DT 13-JUL-1996 (first entry)
XX
DE Antisense DNA to inhibit isoprenyl protein transferase expression.
XX
KW isoprenyl protein transferase; farnesyl; geranyl geranyl; prenylation;
KW inhibition; abnormal; uncontrolled; cell proliferation; cancer;
KW cardiovascular disease; treatment; ss.
XX
OS Synthetic.
XX
PN GB2290791-A.
XX
PD 10-JAN-1996.
XX
PF 29-JUN-1995; 95GB-00013246.
XX
PR 29-JUN-1994; 94GB-00013035.
XX
PA (SCRC) SCRAS SOC CONSEILS RECH APPL SCI.
XX
PI Colote S, Pirotzky E;
XX
DR WPI; 1996-042231/05.
XX
PT Anti-sense oligo-nucleotide(s) hybridising to isoprenyl protein
PT transferase genes - or their transcripts, for treating abnormal or
PT uncontrolled cell proliferation e.g. cancer.
XX
PS Claim 2; Page 13; 27pp; English.
XX
CC AAT11906-41 are antisense oligonucleotides that are selectively
CC hybridisable with a gene or the transcription products for sub-units of
CC isoprenyl protein transferases, pref. farnesyl protein transferase or a
CC gerany geranyl protein transferase. Oligonucleotides contg. these
CC antisense sequences or their derivs. are useful in human or veterinary
CC medicine for treatment of abnormal and/or uncontrolled cell
CC proliferation, e.g. in cases of cardiovascular disease, cancer, viral
CC infections or dermatology. Inhibiting prenylation prevents proteins from
CC binding to active sites on cell membranes, so prevents transduction of
CC extracellular cell signals and thus cell proliferation
XX
SQ Sequence 12 BP; 1 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 32.1%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GTACAGGGA 21
||||||||| |
Db 12 GTACAGGGA 4

RESULT 196
ABH73584
ID ABH73584 standard; DNA; 12 BP.
XX
AC ABH73584;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 273569 for detecting SNP TSC0003234.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is

```
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 273569; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             32.1%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              |||||||||
Db          3 TACGTGTAC 11


RESULT 197
AAV11022
ID   AAV11022 standard; RNA; 13 BP.
XX
AC   AAV11022;
XX
DT   25-MAR-2003  (revised)
DT   14-JUL-1998  (first entry)
XX
DE   Human ribozyme target sequence from HLA-DPB 02DPB #3.
XX
KW   Ribozyme; target; human lymphocyte antigen; HLA-DPB; MHC allele;
KW   major histocompatability complex; cleavage; suppression; transplant;
KW   incompatibility; autoimmune disease; juvenile diabetes;
KW   rheumatoid arthritis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9704087-A1.
XX
PD   06-FEB-1997.
XX
PF   18-JUL-1996;   96WO-EP003173.
XX
PR   18-JUL-1995;   95EP-00111256.
XX
PA   (KRUP/) KRUPP G.
PA   (MARG/) MARGET M.
PA   (WEST/) WESTPHAL E.
PA   (MUEL/) MUELLER-RUCHHOLTZ W.
XX
PI   Krupp G,  Marget M,  Westphal E,  Mueller-Ruchholtz W;
XX
DR   WPI; 1997-132628/12.
XX
PT   Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft
PT   versus host reactions, to overcome blood incompatibility and to treat
PT   auto:immune disease.
XX
PS   Claim 5; Fig 1; 76pp; German.
XX
CC   AAV10915-V11123 are target sequences for a novel ribozyme which cleaves
CC   specific alleles from the major histocompatability complex (MHC). This
CC   ribozyme contains a catalytic region and a hybridisation region which is
CC   complementary to all mRNA transcribed from vertebrate genes of a specific
CC   family of closely related MHC alleles or to mRNA from a single MHC
CC   allele, and is able to cleave such mRNA. The mRNA has a target region
CC   which in case is essentially conserved in all genes of the family but
CC   differs from genes of all other MHC alleles to such a degree that no
CC   cleavage of mRNA transcribed from these other alleles occurs. This allows
CC   the selective reduction or inhibition of expression of all genes of a
CC   family or of a single gene. This ribozyme can be used for permanent or
CC   transient suppression of expression of MHC alleles, in vivo or in vitro.
CC   Specific applications are to prevent guest vs. host or host vs. guest
CC   reactions, to prevent blood incompatibilities (partic. of the ABO, rhesus
CC   and Kell systems) and to treat autoimmune diseases such as juvenile
CC   diabetes and rheumatoid arthritis. The use of this ribozyme avoids the
CC   need for immunosuppressants in transplant patients. It provides very
CC   specific reduction of particular HLA molecules that cause incompatibility
CC   between donor and recipient. (Updated on 25-MAR-2003 to correct PA
CC   field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 13 BP; 3 A; 3 C; 3 G; 0 T; 4 U; 0 Other;

  Query Match             32.1%;  Score 9;  DB 1;  Length 13;
  Best Local Similarity   66.7%;  Pred. No. 2e+02;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              :|||:|:||
Db          1 UACGUGUAC 9


RESULT 198
AAV11018
ID   AAV11018 standard; RNA; 13 BP.
XX
AC   AAV11018;
XX
DT   25-MAR-2003  (revised)
DT   14-JUL-1998  (first entry)
XX
DE   Human ribozyme target sequence from HLA-DPB 01DPB #1.
XX
KW   Ribozyme; target; human lymphocyte antigen; HLA-DPB; MHC allele;
KW   major histocompatability complex; cleavage; suppression; transplant;
KW   incompatibility; autoimmune disease; juvenile diabetes;
KW   rheumatoid arthritis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9704087-A1.
XX
PD   06-FEB-1997.
XX
PF   18-JUL-1996;   96WO-EP003173.
XX
PR   18-JUL-1995;   95EP-00111256.
XX
PA   (KRUP/) KRUPP G.
PA   (MARG/) MARGET M.
PA   (WEST/) WESTPHAL E.
PA   (MUEL/) MUELLER-RUCHHOLTZ W.
XX
PI   Krupp G,  Marget M,  Westphal E,  Mueller-Ruchholtz W;
XX
DR   WPI; 1997-132628/12.
XX
PT   Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft
PT   versus host reactions, to overcome blood incompatibility and to treat
PT   auto:immune disease.
XX
PS   Claim 5; Fig 1; 76pp; German.
XX
CC   AAV10915-V11123 are target sequences for a novel ribozyme which cleaves
CC   specific alleles from the major histocompatability complex (MHC). This
CC   ribozyme contains a catalytic region and a hybridisation region which is
```

```
CC   complementary to all mRNA transcribed from vertebrate genes of a specific
CC   family of closely related MHC alleles or to mRNA from a single MHC
CC   allele, and is able to cleave such mRNA. The mRNA has a target region
CC   which in case is essentially conserved in all genes of the family but
CC   differs from genes of all other MHC alleles to such a degree that no
CC   cleavage of mRNA transcribed from these other alleles occurs. This allows
CC   the selective reduction or inhibition of expression of all genes of a
CC   family or of a single gene. This ribozyme can be used for permanent or
CC   transient suppression of expression of MHC alleles, in vivo or in vitro.
CC   Specific applications are to prevent guest vs. host or host vs. guest
CC   reactions, to prevent blood incompatibilities (partic. of the ABO, rhesus
CC   and Kell systems) and to treat autoimmune diseases such as juvenile
CC   diabetes and rheumatoid arthritis. The use of this ribozyme avoids the
CC   need for immunosuppressants in transplant patients. It provides very
CC   specific reduction of particular HLA molecules that cause incompatibility
CC   between donor and recipient. (Updated on 25-MAR-2003 to correct PA
CC   field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 13 BP; 3 A; 3 C; 3 G; 0 T; 4 U; 0 Other;

  Query Match             32.1%;  Score 9;  DB 1;  Length 13;
  Best Local Similarity   66.7%;  Pred. No. 2e+02;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              :|||:|:||
Db          2 UACGUGUAC 10


RESULT 199
ABC24101/c
ID   ABC24101 standard; DNA; 13 BP.
XX
AC   ABC24101;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 24118 for detecting SNP TSC0005613.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 24118; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             32.1%;  Score 9;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              |||||||||
Db         13 TACGTGTAC 5


RESULT 200
ABC24100
ID   ABC24100 standard; DNA; 13 BP.
XX
AC   ABC24100;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 24117 for detecting SNP TSC0005613.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 24117; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 2 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             32.1%;  Score 9;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              |||||||||
```

```
Db          1 TACGTGTAC 9


RESULT 201
ABC90236
ID   ABC90236 standard; DNA; 13 BP.
XX
AC   ABC90236;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 90253 for detecting SNP TSC0022616.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 90253; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             32.1%;  Score 9;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              |||||||||
Db          4 TACGTGTAC 12


RESULT 202
ABC90237/c
ID   ABC90237 standard; DNA; 13 BP.
XX
AC   ABC90237;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 90254 for detecting SNP TSC0022616.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 90254; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             32.1%;  Score 9;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              |||||||||
Db         10 TACGTGTAC 2


RESULT 203
AAF07226/c
ID   AAF07226 standard; DNA; 17 BP.
XX
AC   AAF07226;
XX
DT   16-FEB-2001  (first entry)
XX
DE   Hammerhead ribozyme substrate #3483.
XX
KW   Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW   interferon alpha; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061729-A2.
XX
PD   19-OCT-2000.
XX
PF   11-APR-2000; 2000WO-US009721.
XX
PR   12-APR-1999;   99US-0129390P.
XX
```

```
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Zwick M,  Pavco P,  Mcswiggen J;
XX
DR   WPI; 2000-647423/62.
XX
PT   Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT   useful for producing e.g. granulocyte colony stimulating factor protein,
PT   interferon alpha and erythropoietin.
XX
PS   Claim 54; Page 136; 164pp; English.
XX
CC   The present invention relates to enzymatic and antisense nucleic acid
CC   molecules that act as inhibitors of the expression of repressor genes
CC   encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC   factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP).
CC   Inhibition of the repressors removes prevents inhibition (and
CC   consequently increases expression of) genes involved in the production of
CC   erythropoietin, granulocyte colony stimulating factor protein and
CC   interferon alpha
XX
SQ   Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             32.1%;  Score 9;  DB 1;  Length 17;
  Best Local Similarity   70.6%;  Pred. No. 2.9e+02;
  Matches   12;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACAGGGAG 22
              ||| |  ||||| | ||
Db         17 CCTCCTGGTACATGTAG 1


RESULT 204
AAZ41850/c
ID   AAZ41850 standard; DNA; 12 BP.
XX
AC   AAZ41850;
XX
DT   20-MAR-2003  (revised)
DT   21-JAN-2000  (first entry)
XX
DE   Organic material detecting primer 211.
XX
KW   Amplification; polymerase chain reaction; PCR; microorganism; compost;
KW   detection; pollutant; soil; food; agricultural chemical; polymer;
KW   organochlorine; primer; ss.
XX
OS   Synthetic.
XX
PN   DE19914461-A1.
XX
PD   21-OCT-1999.
XX
PF   30-MAR-1999;   99DE-01014461.
XX
PR   31-MAR-1998;   98JP-00087651.
PR   16-MAR-1999;   99JP-00069694.
XX
PA   (SAOL ) SANYO ELECTRIC CO LTD.
PA   (NORQ ) SOC TECHNO-INNOVATION AGRIC FORESTY & FI.
XX
PI   Inoue T;
XX
DR   WPI; 1999-592157/51.
XX
PT   Novel polymerase chain reaction method, for differentiating between
PT   microorganisms and for detecting contaminants.
XX
PS   Example 1; Page 22; 78pp; German.
XX
CC   This invention describes a novel method for the amplification of DNA
CC   comprising (i) preparing many primers (P) with different probabilities of
CC   amplification and (ii) simultaneous polymerase chain reaction (PCR) of
CC   many different DNA using these primers. The method is used (i) to
CC   differentiate between different microorganisms in a mixed population and
CC   (ii) to determine presence/absence of an impurity (pollutant), or its
CC   concentration, in e.g. soil, foods, compost etc., typically metals,
CC   agricultural chemicals, polymers, organochlorine compounds etc. A
CC   particular use is monitoring composting of organic material.
CC   Amplification with many primers produces a lot of information, so
CC   reliability of the test is improved, and many samples may be tested
CC   quickly. AAZ41640-Z41855 represent the primers described in the method of
CC   the invention. (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ   Sequence 12 BP; 2 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTAC 16
              || ||||||  ||
Db         12 CCATACGTGCAC 1


RESULT 205
AAZ41634/c
ID   AAZ41634 standard; DNA; 12 BP.
XX
AC   AAZ41634;
XX
DT   19-JAN-2000  (first entry)
XX
DE   Microbe detection in organic waste arbitrarily primed PCR primer #211.
XX
KW   Microbe; detection; organic waste; arbitrarily primer PCR;
KW   random amplified polymorphic DNA; amplification; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   JP11276176-A.
XX
PD   12-OCT-1999.
XX
PF   31-MAR-1998;   98JP-00087652.
XX
PR   31-MAR-1998;   98JP-00087652.
XX
PA   (SAOL ) SANYO ELECTRIC CO LTD.
PA   (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
DR   WPI; 1999-626940/54.
XX
PT   Amplification of a DNA fragment - in order to establish the state of
PT   existence of a microbe.
XX
PS   Example; Page 10; 40pp; Japanese.
XX
CC   A method has been developed for the amplification of a DNA fragment in
CC   which amplification is carried out on the DNA fragments of a number of
CC   different DNAs. The method comprises a PCR reaction repeatedly carrying
CC   out a heat-denaturing step, a primer annealing step and a polymerase
CC   extending step, to amplify the DNA fragments of a plural of different
CC   DNAs. The method can detect the existence of a microbe in organic waste.
CC   AAZ41424 to AAZ41639 represent PCR primers used in random amplified
CC   polymorphic DNA arbitrarily primed PCR, for the detection of microbes in
CC   organic waste
XX
SQ   Sequence 12 BP; 2 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTAC 16
              || ||||||  ||
```

```
Db         12 CCATACGTGCAC 1


RESULT 206
AAC97985/c
ID   AAC97985 standard; DNA; 12 BP.
XX
AC   AAC97985;
XX
DT   28-FEB-2001  (first entry)
XX
DE   Primer used to illustrate DNA amplification method SEQ ID 211.
XX
KW   Primer; amplification; selective; ss.
XX
OS   Synthetic.
XX
PN   JP2000270867-A.
XX
PD   03-OCT-2000.
XX
PF   19-MAR-1999;   99JP-00076844.
XX
PR   19-MAR-1999;   99JP-00076844.
XX
PA   (SAOL ) SANYO ELECTRIC CO LTD.
PA   (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
DR   WPI; 2001-011047/02.
XX
PT   Amplification of a DNA fragment and its apparatus.
XX
PS   Example 1; Page 11; 32pp; Japanese.
XX
CC   This invention relates to a method for amplifying a DNA fragment. The
CC   method comprises successive repetitions of heat-denaturing, annealing of
CC   a primer and an extending step using a DNA polymerase. The method makes
CC   use of a cDNA pool in which the primer is one primer or a pair of primer
CC   sets and has an amplification probability which allows it to amplify a
CC   DNA fragment from a limited number of the cDNAs among the DNA pool (where
CC   the limited number is in the range of 1 to 25). Also included in the
CC   invention are apparatus used for carrying out the method, a primer and a
CC   DNA polymerase and a kit used for amplifying a DNA fragment. The method
CC   can be used to amplify a limited number of cDNAs from a pool in which a
CC   wide variety of cDNAs are present. Oligonucleotides AAC97775 - AAC97990
CC   represent primers used in an example illustrating the method of the
CC   invention
XX
SQ   Sequence 12 BP; 2 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTAC 16
              || |||||| ||
Db         12 CCATACGTGCAC 1


RESULT 207
ABH71898
ID   ABH71898 standard; DNA; 12 BP.
XX
AC   ABH71898;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 271875 for detecting SNP TSC0002640.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 271875; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              |||||| ||||
Db          1 CCTACGATTACA 12


RESULT 208
ABI23374
ID   ABI23374 standard; DNA; 12 BP.
XX
AC   ABI23374;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 323347 for detecting SNP TSC0031342.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
```

```
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 323347; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              ||||||||  ||
Db          1 TACGTGTAGGGG 12


RESULT 209
ABI26921/c
ID   ABI26921 standard; DNA; 12 BP.
XX
AC   ABI26921;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 326894 for detecting SNP TSC0033327.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 326894; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
              || || ||||||
Db         12 GTTTATAGGGAG 1


RESULT 210
ABI17179/c
ID   ABI17179 standard; DNA; 12 BP.
XX
AC   ABI17179;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 317152 for detecting SNP TSC0027831.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 317152; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
```

```
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
              ||||  ||||||
Db         12 TGTAGGGGGAGT 1


RESULT 211
ABH71301
ID   ABH71301 standard; DNA; 12 BP.
XX
AC   ABH71301;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 271278 for detecting SNP TSC0002450.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 271278; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              ||| ||| ||||
Db          1 CCTTCGTATACA 12


RESULT 212
ABH73583/c
ID   ABH73583 standard; DNA; 12 BP.
XX
AC   ABH73583;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 273568 for detecting SNP TSC0003234.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 273568; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              | |||| |||||
Db         12 CATACGCGTACA 1


RESULT 213
ABH75458
ID   ABH75458 standard; DNA; 12 BP.
XX
AC   ABH75458;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 275449 for detecting SNP TSC0003897.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
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XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 275449; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
               |||  |||||||
Db          1 TGTTTAGGGAGT 12


RESULT 214
ABI10854/c
ID   ABI10854 standard; DNA; 12 BP.
XX
AC   ABI10854;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 310827 for detecting SNP TSC0024134.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 310827; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
              || || ||||||
Db         12 GTATATAGGGAG 1


RESULT 215
ABI37455
ID   ABI37455 standard; DNA; 12 BP.
XX
AC   ABI37455;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 337428 for detecting SNP TSC0039870.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 337428; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
```

```
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
              |||| | |||||
Db          1 TGTAGAAGGAGT 12


RESULT 216
ABI00095
ID   ABI00095 standard; DNA; 12 BP.
XX
AC   ABI00095;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 300068 for detecting SNP TSC0018851.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 300068; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGA 21
              ||||||  ||||
Db          1 CGTGTAGCGGGA 12


RESULT 217
ABI68722/c
ID   ABI68722 standard; DNA; 12 BP.
XX
AC   ABI68722;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 368695 for detecting SNP TSC0057163.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 368695; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
              || | |||||||
Db         12 TGGAAAGGGAGT 1


RESULT 218
ABI72643/c
ID   ABI72643 standard; DNA; 12 BP.
XX
AC   ABI72643;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 372616 for detecting SNP TSC0059501.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
```

```
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 372616; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
              |||| | |||||
Db         12 TGTATATGGAGT 1


RESULT 219
ABI59103/c
ID   ABI59103 standard; DNA; 12 BP.
XX
AC   ABI59103;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 359076 for detecting SNP TSC0010484.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 359076; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
              ||||| |||||
Db         12 GTGTATTGGGAG 1


RESULT 220
ABI19821
ID   ABI19821 standard; DNA; 12 BP.
XX
AC   ABI19821;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 319794 for detecting SNP TSC0029404.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 319794; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
```

```
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 1 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTCCAGG 28
              ||||| || |||
Db          1 AGGGATTCGAGG 12


RESULT 221
ABH70982/c
ID   ABH70982 standard; DNA; 12 BP.
XX
AC   ABH70982;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 270959 for detecting SNP TSC0002339.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 270959; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
              ||||  ||||||
Db         12 TGTAATGGGAGT 1


RESULT 222
ABI28323
ID   ABI28323 standard; DNA; 12 BP.
XX
AC   ABI28323;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 328296 for detecting SNP TSC0034221.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 328296; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
              |||| || ||||
Db          1 TGTAGAGAGAGT 12


RESULT 223
ABH73586/c
ID   ABH73586 standard; DNA; 12 BP.
```

```
XX
AC   ABH73586;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 273571 for detecting SNP TSC0003234.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 273571; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              | ||||  |||||
Db         12 CGTACGCGTACA 1


RESULT 224
ABH81956/c
ID   ABH81956 standard; DNA; 12 BP.
XX
AC   ABH81956;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 281949 for detecting SNP TSC0010190.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 281949; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTCCAGG 28
              |||||||  |||
Db         12 AGGGAGTTAAGG 1


RESULT 225
ABI18399
ID   ABI18399 standard; DNA; 12 BP.
XX
AC   ABI18399;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 318372 for detecting SNP TSC0028620.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
```

```
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 318372; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              ||||| | ||||
Db          1 CCTACCTCTACA 12


RESULT 226
ABI00093
ID   ABI00093 standard; DNA; 12 BP.
XX
AC   ABI00093;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 300066 for detecting SNP TSC0018851.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 300066; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGA 21
              ||||||  ||||
Db          1 CGTGTAGTGGGA 12


RESULT 227
ABH84553
ID   ABH84553 standard; DNA; 12 BP.
XX
AC   ABH84553;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 284546 for detecting SNP TSC0011875.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 284546; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy          11 GTGTACAGGGAG 22
               | ||| ||||||
Db           1 GAGTATAGGGAG 12
```

RESULT 228
ABI55944
ID ABI55944 standard; DNA; 12 BP.
XX
AC ABI55944;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 355917 for detecting SNP TSC0049869.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 355917; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match   31.4%; Score 8.8; DB 1; Length 12;
  Best Local Similarity   83.3%; Pred. No. 2e+02;
  Matches   10; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

```
Qy          12 TGTACAGGGAGT 23
               |||  |||||||
Db           1 TGTGGAGGGAGT 12
```

RESULT 229
ABI01714
ID ABI01714 standard; DNA; 12 BP.
XX
AC ABI01714;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 301687 for detecting SNP TSC0019610.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 301687; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 1 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match   31.4%; Score 8.8; DB 1; Length 12;
  Best Local Similarity   83.3%; Pred. No. 2e+02;
  Matches   10; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

```
Qy          10 CGTGTACAGGGA 21
               |||||  |||||
Db           1 CGTGTTTAGGGA 12
```

RESULT 230
ABH99794
ID ABH99794 standard; DNA; 12 BP.
XX
AC ABH99794;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 299787 for detecting SNP TSC0018744.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.

```
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 299787; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          11 GTGTACAGGGAG 22
               | ||| ||||||
Db           1 GAGTAGAGGGAG 12


RESULT 231
ABH72448
ID   ABH72448 standard; DNA; 12 BP.
XX
AC   ABH72448;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 272433 for detecting SNP TSC0002816.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 272433; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           6 CCTACGTGTACA 17
               ||||| | ||||
Db           1 CCTACATATACA 12


RESULT 232
ABH79191
ID   ABH79191 standard; DNA; 12 BP.
XX
AC   ABH79191;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 279184 for detecting SNP TSC0007020.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 279184; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
```

```
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              ||||||| || |
Db          1 CCTACGTTTAAA 12


RESULT 233
ABI78777
ID   ABI78777 standard; DNA; 12 BP.
XX
AC   ABI78777;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 378750 for detecting SNP TSC0062918.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 378750; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
              |||| ||||| |
Db          1 TGTAAAGGGAAT 12


RESULT 234
ABH82234/c
ID   ABH82234 standard; DNA; 12 BP.
XX
AC   ABH82234;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 282227 for detecting SNP TSC0010599.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 282227; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
              ||||  ||||||
Db         12 GTGTTTAGGGAG 1


RESULT 235
ADB81359
ID   ADB81359 standard; DNA; 12 BP.
XX
AC   ADB81359;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Bacteriophage C31-Integrase 3' splice acceptor consensus DNA (868-879).
XX
KW   ss; phiC31 integrase; site specific recombinase; SSR; gene function;
KW   disease model; gene therapy; transgenic; C31-Int.
XX
```

OS Bacteriophage phi-C31.
XX
PN WO2003066867-A2.
XX
PD 14-AUG-2003.
XX
PF 05-FEB-2003; 2003WO-EP001122.
XX
PR 06-FEB-2002; 2002US-0354741P.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
XX
PI Andreas S, Faust N;
XX
DR WPI; 2003-663599/62.
XX
PT New genetically engineered nucleic acid molecule, useful for preparing an
PT agent for recombining a DNA molecule containing phiC31 integrase
PT recognition sequences in a eukaryotic cell, a vertebrate or transgenic
PT organism.
XX
PS Example 1; Page 16; 87pp; English.
XX
CC This invention relates to novel genetically engineered nucleic acid
CC molecules encoding phiC31 integrase (C31-Int), which has been codon
CC optimised for expression in eukaryotic host cells. The phiC31 integrase
CC is a site specific recombinase (SSR) that catalyzes recombination between
CC two phiC31 recognition sequences. The introduction of silent mutations
CC into the coding sequence changes the given codon to one that is most
CC frequently used in the respective host, which in turn alters expression
CC levels. Accordingly, using this ability to generate controlled and
CC permanent modifications in eukaryotic genomes has various research
CC applications including the study of gene function and the creation of
CC disease models, as well as gene therapy for medical applications, and the
CC design of economically important animals and crops. Furthermore, the
CC phiC31 integrase of the invention is useful for preparing an agent for
CC recombining a DNA molecule containing phiC31 integrase recognition
CC sequences in a eukaryotic cell, a vertebrate or transgenic organism. This
CC oligonucleotide sequence is a bacteriophage phi-C31 3' splice acceptor
CC consensus DNA sequence found at positions 868-879 and a target for silent
CC mutations of the invention.
XX
SQ Sequence 12 BP; 3 A; 4 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 31.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 17 AGGGAGTCCAGG 28
||||| |||||
Db 1 AGGGACCCCAGG 12

RESULT 236
AAV11023
ID AAV11023 standard; RNA; 13 BP.
XX
AC AAV11023;
XX
DT 25-MAR-2003 (revised)
DT 14-JUL-1998 (first entry)
XX
DE Human ribozyme target sequence from HLA-DPB 03DPB #1.
XX
KW Ribozyme; target; human lymphocyte antigen; HLA-DPB; MHC allele;
KW major histocompatability complex; cleavage; suppression; transplant;
KW incompatibility; autoimmune disease; juvenile diabetes;
KW rheumatoid arthritis; ss.
XX
OS Homo sapiens.
XX
PN WO9704087-A1.
XX
PD 06-FEB-1997.
XX
PF 18-JUL-1996; 96WO-EP003173.
XX
PR 18-JUL-1995; 95EP-00111256.
XX
PA (KRUP/) KRUPP G.
PA (MARG/) MARGET M.
PA (WEST/) WESTPHAL E.
PA (MUEL/) MUELLER-RUCHHOLTZ W.
XX
PI Krupp G, Marget M, Westphal E, Mueller-Ruchholtz W;
XX
DR WPI; 1997-132628/12.
XX
PT Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft
PT versus host reactions, to overcome blood incompatibility and to treat
PT auto:immune disease.
XX
PS Claim 5; Fig 1; 76pp; German.
XX
CC AAV10915-V11123 are target sequences for a novel ribozyme which cleaves
CC specific alleles from the major histocompatability complex (MHC). This
CC ribozyme contains a catalytic region and a hybridisation region which is
CC complementary to all mRNA transcribed from vertebrate genes of a specific
CC family of closely related MHC alleles or to mRNA from a single MHC
CC allele, and is able to cleave such mRNA. The mRNA has a target region
CC which in case is essentially conserved in all genes of the family but
CC differs from genes of all other MHC alleles to such a degree that no
CC cleavage of mRNA transcribed from these other alleles occurs. This allows
CC the selective reduction or inhibition of expression of all genes of a
CC family or of a single gene. This ribozyme can be used for permanent or
CC transient suppression of expression of MHC alleles, in vivo or in vitro.
CC Specific applications are to prevent guest vs. host or host vs. guest
CC reactions, to prevent blood incompatibilities (partic. of the ABO, rhesus
CC and Kell systems) and to treat autoimmune diseases such as juvenile
CC diabetes and rheumatoid arthritis. The use of this ribozyme avoids the
CC need for immunosuppressants in transplant patients. It provides very
CC specific reduction of particular HLA molecules that cause incompatibility
CC between donor and recipient. (Updated on 25-MAR-2003 to correct PA
CC field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 13 BP; 3 A; 3 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 31.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 9 ACGTGTACAGGG 20
||| | | || ||
Db 1 ACGUGUACCAGG 12

RESULT 237
AAV11115
ID AAV11115 standard; RNA; 13 BP.
XX
AC AAV11115;
XX
DT 25-MAR-2003 (revised)
DT 14-JUL-1998 (first entry)
XX
DE Human ribozyme target sequence from HLA-DRB 19DRB #5.
XX
KW Ribozyme; target; human lymphocyte antigen; HLA-DRB; MHC allele;
KW major histocompatability complex; cleavage; suppression; transplant;
KW incompatibility; autoimmune disease; juvenile diabetes;
KW rheumatoid arthritis; ss.
XX
OS Homo sapiens.
XX
PN WO9704087-A1.
XX

```
PD   06-FEB-1997.
XX
PF   18-JUL-1996;   96WO-EP003173.
XX
PR   18-JUL-1995;   95EP-00111256.
XX
PA   (KRUP/) KRUPP G.
PA   (MARG/) MARGET M.
PA   (WEST/) WESTPHAL E.
PA   (MUEL/) MUELLER-RUCHHOLTZ W.
XX
PI   Krupp G,  Marget M,  Westphal E,  Mueller-Ruchholtz W;
XX
DR   WPI; 1997-132628/12.
XX
PT   Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft
PT   versus host reactions, to overcome blood incompatibility and to treat
PT   auto:immune disease.
XX
PS   Claim 5; Fig 1; 76pp; German.
XX
CC   AAV10915-V11123 are target sequences for a novel ribozyme which cleaves
CC   specific alleles from the major histocompatability complex (MHC). This
CC   ribozyme contains a catalytic region and a hybridisation region which is
CC   complementary to all mRNA transcribed from vertebrate genes of a specific
CC   family of closely related MHC alleles or to mRNA from a single MHC
CC   allele, and is able to cleave such mRNA. The mRNA has a target region
CC   which in case is essentially conserved in all genes of the family but
CC   differs from genes of all other MHC alleles to such a degree that no
CC   cleavage of mRNA transcribed from these other alleles occurs. This allows
CC   the selective reduction or inhibition of expression of all genes of a
CC   family or of a single gene. This ribozyme can be used for permanent or
CC   transient suppression of expression of MHC alleles, in vivo or in vitro.
CC   Specific applications are to prevent guest vs. host or host vs. guest
CC   reactions, to prevent blood incompatibilities (partic. of the ABO, rhesus
CC   and Kell systems) and to treat autoimmune diseases such as juvenile
CC   diabetes and rheumatoid arthritis. The use of this ribozyme avoids the
CC   need for immunosuppressants in transplant patients. It provides very
CC   specific reduction of particular HLA molecules that cause incompatibility
CC   between donor and recipient. (Updated on 25-MAR-2003 to correct PA
CC   field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 13 BP; 4 A; 3 C; 5 G; 0 T; 1 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   75.0%;  Pred. No. 2.3e+02;
  Matches    9;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTCCAGG 28
              ||||| :|| ||
Db          1 AGGGAAUCCCGG 12


RESULT 238
AAV11113/c
ID   AAV11113 standard; RNA; 13 BP.
XX
AC   AAV11113;
XX
DT   25-MAR-2003  (revised)
DT   14-JUL-1998  (first entry)
XX
DE   Human ribozyme target sequence from HLA-DRB 19DRB #3.
XX
KW   Ribozyme; target; human lymphocyte antigen; HLA-DRB; MHC allele;
KW   major histocompatability complex; cleavage; suppression; transplant;
KW   incompatibility; autoimmune disease; juvenile diabetes;
KW   rheumatoid arthritis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9704087-A1.
XX
```

```
PD   06-FEB-1997.
XX
PF   18-JUL-1996;   96WO-EP003173.
XX
PR   18-JUL-1995;   95EP-00111256.
XX
PA   (KRUP/) KRUPP G.
PA   (MARG/) MARGET M.
PA   (WEST/) WESTPHAL E.
PA   (MUEL/) MUELLER-RUCHHOLTZ W.
XX
PI   Krupp G,  Marget M,  Westphal E,  Mueller-Ruchholtz W;
XX
DR   WPI; 1997-132628/12.
XX
PT   Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft
PT   versus host reactions, to overcome blood incompatibility and to treat
PT   auto:immune disease.
XX
PS   Claim 5; Fig 1; 76pp; German.
XX
CC   AAV10915-V11123 are target sequences for a novel ribozyme which cleaves
CC   specific alleles from the major histocompatability complex (MHC). This
CC   ribozyme contains a catalytic region and a hybridisation region which is
CC   complementary to all mRNA transcribed from vertebrate genes of a specific
CC   family of closely related MHC alleles or to mRNA from a single MHC
CC   allele, and is able to cleave such mRNA. The mRNA has a target region
CC   which in case is essentially conserved in all genes of the family but
CC   differs from genes of all other MHC alleles to such a degree that no
CC   cleavage of mRNA transcribed from these other alleles occurs. This allows
CC   the selective reduction or inhibition of expression of all genes of a
CC   family or of a single gene. This ribozyme can be used for permanent or
CC   transient suppression of expression of MHC alleles, in vivo or in vitro.
CC   Specific applications are to prevent guest vs. host or host vs. guest
CC   reactions, to prevent blood incompatibilities (partic. of the ABO, rhesus
CC   and Kell systems) and to treat autoimmune diseases such as juvenile
CC   diabetes and rheumatoid arthritis. The use of this ribozyme avoids the
CC   need for immunosuppressants in transplant patients. It provides very
CC   specific reduction of particular HLA molecules that cause incompatibility
CC   between donor and recipient. (Updated on 25-MAR-2003 to correct PA
CC   field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 13 BP; 3 A; 3 C; 4 G; 0 T; 3 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGTCC 25
              | |||| |||||
Db         13 TCCAGGAAGTCC 2


RESULT 239
AAV11114
ID   AAV11114 standard; RNA; 13 BP.
XX
AC   AAV11114;
XX
DT   25-MAR-2003  (revised)
DT   14-JUL-1998  (first entry)
XX
DE   Human ribozyme target sequence from HLA-DRB 19DRB #4.
XX
KW   Ribozyme; target; human lymphocyte antigen; HLA-DRB; MHC allele;
KW   major histocompatability complex; cleavage; suppression; transplant;
KW   incompatibility; autoimmune disease; juvenile diabetes;
KW   rheumatoid arthritis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9704087-A1.
XX
```

```
PD   06-FEB-1997.
XX
PF   18-JUL-1996;   96WO-EP003173.
XX
PR   18-JUL-1995;   95EP-00111256.
XX
PA   (KRUP/) KRUPP G.
PA   (MARG/) MARGET M.
PA   (WEST/) WESTPHAL E.
PA   (MUEL/) MUELLER-RUCHHOLTZ W.
XX
PI   Krupp G,  Marget M,  Westphal E,  Mueller-Ruchholtz W;
XX
DR   WPI; 1997-132628/12.
XX
PT   Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft
PT   versus host reactions, to overcome blood incompatibility and to treat
PT   auto:immune disease.
XX
PS   Claim 5; Fig 1; 76pp; German.
XX
CC   AAV10915-V11123 are target sequences for a novel ribozyme which cleaves
CC   specific alleles from the major histocompatability complex (MHC). This
CC   ribozyme contains a catalytic region and a hybridisation region which is
CC   complementary to all mRNA transcribed from vertebrate genes of a specific
CC   family of closely related MHC alleles or to mRNA from a single MHC
CC   allele, and is able to cleave such mRNA. The mRNA has a target region
CC   which in case is essentially conserved in all genes of the family but
CC   differs from genes of all other MHC alleles to such a degree that no
CC   cleavage of mRNA transcribed from these other alleles occurs. This allows
CC   the selective reduction or inhibition of expression of all genes of a
CC   family or of a single gene. This ribozyme can be used for permanent or
CC   transient suppression of expression of MHC alleles, in vivo or in vitro.
CC   Specific applications are to prevent guest vs. host or host vs. guest
CC   reactions, to prevent blood incompatibilities (partic. of the ABO, rhesus
CC   and Kell systems) and to treat autoimmune diseases such as juvenile
CC   diabetes and rheumatoid arthritis. The use of this ribozyme avoids the
CC   need for immunosuppressants in transplant patients. It provides very
CC   specific reduction of particular HLA molecules that cause incompatibility
CC   between donor and recipient. (Updated on 25-MAR-2003 to correct PA
CC   field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 13 BP; 4 A; 2 C; 5 G; 0 T; 2 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   75.0%;  Pred. No. 2.3e+02;
  Matches    9;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTCCAGG 28
              ||||| :|| ||
Db          1 AGGGAAUCCUGG 12


RESULT 240
ABC25956/c
ID   ABC25956 standard; DNA; 13 BP.
XX
AC   ABC25956;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 25973 for detecting SNP TSC0006663.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 25973; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 1 C; 3 G; 4 T; 0 U; 1 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              ||||||| || |
Db         12 CCTACGTTTAAA 1


RESULT 241
ABC37721/c
ID   ABC37721 standard; DNA; 13 BP.
XX
AC   ABC37721;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 37738 for detecting SNP TSC0011735.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
```

```
XX
PS   Claim 1; SEQ ID NO 37738; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 3 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              ||||| || |||
Db         12 TACGTATATAGG 1


RESULT 242
ABF36729/c
ID   ABF36729 standard; DNA; 13 BP.
XX
AC   ABF36729;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 136726 for detecting SNP TSC0034175.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 136726; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 4 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAGT 23
               |||| | |||||
Db          13 TGTAAATGGAGT 2


RESULT 243
ABF77240/c
ID   ABF77240 standard; DNA; 13 BP.
XX
AC   ABF77240;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 177237 for detecting SNP TSC0043944.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 177237; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTAC 16
              |||||||| | |
Db         12 CCCTACGTCTTC 1
```

```
RESULT 244
ABH11994
ID   ABH11994 standard; DNA; 13 BP.
XX
AC   ABH11994;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 211971 for detecting SNP TSC0051670.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 211971; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 1 A; 1 C; 8 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          11 GTGTACAGGGAG 22
               |||| | |||||
Db           2 GTGTGCGGGGAG 13


RESULT 245
ABH11995/c
ID   ABH11995 standard; DNA; 13 BP.
XX
AC   ABH11995;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 211972 for detecting SNP TSC0051670.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 211972; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 8 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          11 GTGTACAGGGAG 22
               |||| | |||||
Db          12 GTGTGCGGGGAG 1


RESULT 246
ABC25957
ID   ABC25957 standard; DNA; 13 BP.
XX
AC   ABC25957;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 25974 for detecting SNP TSC0006663.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
```

XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 25974; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 3 C; 1 G; 4 T; 0 U; 1 Other;

Query Match 31.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CCTACGTGTACA 17
||||||| || |
Db 2 CCTACGTTTAAA 13

RESULT 247
ABC05016/c
ID ABC05016 standard; DNA; 13 BP.
XX
AC ABC05016;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 5007 for detecting SNP TSC0001738.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 5007; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 31.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CCCTACGTGTAC 16
||||||| |||
Db 12 CCCTACGATTAC 1

RESULT 248
ABC59500
ID ABC59500 standard; DNA; 13 BP.
XX
AC ABC59500;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 59517 for detecting SNP TSC0015944.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 59517; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 0 C; 4 G; 4 T; 0 U; 0 Other;

```
  Query Match            31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity  83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
              | || |||||||
Db          1 TATAAAGGGAGT 12


RESULT 249
ABC37805/c
ID   ABC37805 standard; DNA; 13 BP.
XX
AC   ABC37805;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 37822 for detecting SNP TSC0011747.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 37822; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match            31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity  83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
              | || |||||||
Db         13 TTTAGAGGGAGT 2


RESULT 250
ABC64857/c
ID   ABC64857 standard; DNA; 13 BP.
XX
AC   ABC64857;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 64874 for detecting SNP TSC0017093.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 64874; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 1 A; 9 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match            31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity  83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
              | ||| ||||||
Db         12 GGGTAGAGGGAG 1


RESULT 251
ABC64858
ID   ABC64858 standard; DNA; 13 BP.
XX
AC   ABC64858;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 64875 for detecting SNP TSC0017093.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
```

```
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 64875; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 8 G; 2 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
              |||| ||||||
Db          2 GGGTATAGGGAG 13


RESULT 252
ABF21570
ID   ABF21570 standard; DNA; 13 BP.
XX
AC   ABF21570;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 121567 for detecting SNP TSC0030367.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 121567; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
              |||| || ||||
Db          1 TGTATAGAGAGT 12


RESULT 253
ABF77241
ID   ABF77241 standard; DNA; 13 BP.
XX
AC   ABF77241;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 177238 for detecting SNP TSC0043944.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 177238; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
```

```
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 1 A; 6 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity  83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTAC 16
              |||||||| | |
Db          2 CCCTACGTCTTC 13


RESULT 254
ABF60519/c
ID   ABF60519 standard; DNA; 13 BP.
XX
AC   ABF60519;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 160516 for detecting SNP TSC0040412.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 160516; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity  83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
               ||||| | ||||
Db         12 GTGTAGAAGGAG 1


RESULT 255
ABF87825/c
ID   ABF87825 standard; DNA; 13 BP.
XX
AC   ABF87825;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 187822 for detecting SNP TSC0001439.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 187822; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 7 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity  83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
               ||||  ||||||
Db         12 GTGTTGAGGGAG 1


RESULT 256
ABF89999/c
ID   ABF89999 standard; DNA; 13 BP.
XX
AC   ABF89999;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 189996 for detecting SNP TSC0046736.
```

```
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 189996; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 4 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAGT 23
               | || |||||||
Db          13 TATATAGGGAGT 2


RESULT 257
ABF91303/c
ID   ABF91303 standard; DNA; 13 BP.
XX
AC   ABF91303;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 191300 for detecting SNP TSC0047061.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 191300; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAGT 23
               | || |||||||
Db          12 TTTAAAGGGAGT 1


RESULT 258
ABC64856
ID   ABC64856 standard; DNA; 13 BP.
XX
AC   ABC64856;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 64873 for detecting SNP TSC0017093.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 64873; 29pp + Sequence Listing; German.
```

```
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 9 G; 1 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
              | ||| ||||||
Db          2 GGGTAGAGGGAG 13


RESULT 259
ABF74652/c
ID   ABF74652 standard; DNA; 13 BP.
XX
AC   ABF74652;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 174649 for detecting SNP TSC0009116.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 174649; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 1 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTAC 16
              |||||||  ||
Db         13 CCCTACGTAAAC 2


RESULT 260
ABH30582
ID   ABH30582 standard; DNA; 13 BP.
XX
AC   ABH30582;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 230559 for detecting SNP TSC0056234.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 230559; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              |||||||| | |
Db          2 TACGTGTATACG 13


RESULT 261
```

```
ABH48420/c
ID   ABH48420 standard; DNA; 13 BP.
XX
AC   ABH48420;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 248397 for detecting SNP TSC0060697.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 248397; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 1 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTAC 16
              ||||||||  ||
Db         13 CCCTACGTAAAC 2


RESULT 262
ABH48421
ID   ABH48421 standard; DNA; 13 BP.
XX
AC   ABH48421;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 248398 for detecting SNP TSC0060697.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 248398; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTAC 16
              ||||||||  ||
Db          1 CCCTACGTAAAC 12


RESULT 263
ABC49804/c
ID   ABC49804 standard; DNA; 13 BP.
XX
AC   ABC49804;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 49821 for detecting SNP TSC0014053.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
```

```
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 49821; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 2 C; 4 G; 4 T; 0 U; 1 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              | ||||| |||||
Db         12 CATACGCGTACA 1


RESULT 264
ABC49805
ID   ABC49805 standard; DNA; 13 BP.
XX
AC   ABC49805;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 49822 for detecting SNP TSC0014053.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 49822; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 4 C; 2 G; 2 T; 0 U; 1 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              | ||||| |||||
Db          2 CATACGCGTACA 13


RESULT 265
ABH64062/c
ID   ABH64062 standard; DNA; 13 BP.
XX
AC   ABH64062;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 264039 for detecting SNP TSC0005398.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 264039; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 1 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
```

```
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              ||||||| |||
Db         12 CCTACGTAAACA 1


RESULT 266
ABC11970
ID   ABC11970 standard; DNA; 13 BP.
XX
AC   ABC11970;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 11977 for detecting SNP TSC0002871.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 11977; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTCCAGG 28
              ||||||| |||
Db          2 AGGGAGTGTAGG 13


RESULT 267
ABC37715/c
ID   ABC37715 standard; DNA; 13 BP.
XX
AC   ABC37715;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 37732 for detecting SNP TSC0011735.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 37732; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              || ||||| |||
Db         12 TATGTGTATAGG 1


RESULT 268
ABC62971/c
ID   ABC62971 standard; DNA; 13 BP.
XX
AC   ABC62971;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 62988 for detecting SNP TSC0016657.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
```

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XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 62988; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          10 CGTGTACAGGGA 21
               |||||| ||| |
Db          13 CGTGTAAAGGTA 2


RESULT 269
ABF59322
ID   ABF59322 standard; DNA; 13 BP.
XX
AC   ABF59322;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 159319 for detecting SNP TSC0040109.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 159319; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAGT 23
               | || |||||||
Db           1 TTTATAGGGAGT 12


RESULT 270
ABF60516
ID   ABF60516 standard; DNA; 13 BP.
XX
AC   ABF60516;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 160513 for detecting SNP TSC0040412.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 160513; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
```

```
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
              ||||| | ||||
Db          2 GTGTAAAAGGAG 13


RESULT 271
ABH37108/c
ID   ABH37108 standard; DNA; 13 BP.
XX
AC   ABH37108;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 237085 for detecting SNP TSC0057833.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 237085; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 1 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              ||||||  ||||
Db         12 CCTACGAATACA 1


RESULT 272
ABF87824
ID   ABF87824 standard; DNA; 13 BP.
XX
AC   ABF87824;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 187821 for detecting SNP TSC0001439.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 187821; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 0 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
              ||||  ||||||
Db          2 GTGTTGAGGGAG 13


RESULT 273
ABC76137/c
ID   ABC76137 standard; DNA; 13 BP.
XX
AC   ABC76137;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 76154 for detecting SNP TSC0019495.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
```

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 76154; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 31.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TACGTGTACAGG 19
| |||||| |||
Db 12 TGCGTGTAAAGG 1

RESULT 274
ABC56486/c
ID ABC56486 standard; DNA; 13 BP.
XX
AC ABC56486;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 56503 for detecting SNP TSC0015314.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 56503; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 1 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 31.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CCCTACGTGTAC 16
| |||||| |||
Db 13 CACTACGTTTAC 2

RESULT 275
ABC60698
ID ABC60698 standard; DNA; 13 BP.
XX
AC ABC60698;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 60715 for detecting SNP TSC0016198.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 60715; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic

```
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 0 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
              ||||  ||||||
Db          1 GTGTTTAGGGAG 12


RESULT 276
ABC37725/c
ID   ABC37725 standard; DNA; 13 BP.
XX
AC   ABC37725;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 37742 for detecting SNP TSC0011735.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 37742; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              |||| ||| |||
Db         12 TACGCGTATAGG 1


RESULT 277
ABC62970
ID   ABC62970 standard; DNA; 13 BP.
XX
AC   ABC62970;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 62987 for detecting SNP TSC0016657.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 62987; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGA 21
              |||||| ||| |
Db          1 CGTGTAAAGGTA 12


RESULT 278
ABF36730
ID   ABF36730 standard; DNA; 13 BP.
```

```
XX
AC   ABF36730;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 136727 for detecting SNP TSC0034175.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 136727; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity  83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
               |||| | |||||
Db          1 TGTAAACGGAGT 12


RESULT 279
ABF36731/c
ID   ABF36731 standard; DNA; 13 BP.
XX
AC   ABF36731;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 136728 for detecting SNP TSC0034175.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 136728; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity  83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
               |||| | |||||
Db         13 TGTAAACGGAGT 2


RESULT 280
ABF82918/c
ID   ABF82918 standard; DNA; 13 BP.
XX
AC   ABF82918;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 182915 for detecting SNP TSC0045193.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
```

```
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 182915; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match          31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        6 CCTACGTGTACA 17
            ||||| | ||||
Db       13 CCTACATATACA 2


RESULT 281
ABC85926
ID   ABC85926 standard; DNA; 13 BP.
XX
AC   ABC85926;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 85943 for detecting SNP TSC0021600.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 85943; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match          31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        12 TGTACAGGGAGT 23
               |||| |||| ||
Db         1 TGTAAAGGGTGT 12


RESULT 282
ABC37714
ID   ABC37714 standard; DNA; 13 BP.
XX
AC   ABC37714;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 37731 for detecting SNP TSC0011735.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 37731; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match          31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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```
Qy          8 TACGTGTACAGG 19
              || ||||| |||
Db          2 TATGTGTATAGG 13
```

RESULT 283
ABC37724
ID ABC37724 standard; DNA; 13 BP.
XX
AC ABC37724;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 37741 for detecting SNP TSC0011735.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 37741; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

```
  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              |||| ||| |||
Db          2 TACGCGTATAGG 13
```

RESULT 284
ABF40375
ID ABF40375 standard; DNA; 13 BP.
XX
AC ABF40375;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 140372 for detecting SNP TSC0035182.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 140372; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

```
  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTAC 16
              |||||||| | |
Db          2 CCCTACGTATCC 13
```

RESULT 285
ABF97836/c
ID ABF97836 standard; DNA; 13 BP.
XX
AC ABF97836;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 197833 for detecting SNP TSC0048686.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.

XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 197833; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 31.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CCCTACGTGTAC 16
|| |||||| |||
Db 12 CTCTACGTCTAC 1

RESULT 286
ABF87826
ID ABF87826 standard; DNA; 13 BP.
XX
AC ABF87826;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 187823 for detecting SNP TSC0001439.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 187823; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 31.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GTGTACAGGGAG 22
|||| ||||||
Db 2 GTGTTAAGGGAG 13

RESULT 287
ABF91302
ID ABF91302 standard; DNA; 13 BP.
XX
AC ABF91302;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 191299 for detecting SNP TSC0047061.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 191299; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at

```
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
              | || |||||||
Db          2 TTTAAAGGGAGT 13


RESULT 288
ABC57873/c
ID   ABC57873 standard; DNA; 13 BP.
XX
AC   ABC57873;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 57890 for detecting SNP TSC0015568.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 57890; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              |||||||| | |
Db         13 TACGTGTAGATG 2


RESULT 289
ABC62969/c
ID   ABC62969 standard; DNA; 13 BP.
XX
AC   ABC62969;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 62986 for detecting SNP TSC0016657.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 62986; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGA 21
              |||||| ||| |
Db         13 CGTGTAGAGGTA 2


RESULT 290
ABH35428
ID   ABH35428 standard; DNA; 13 BP.
XX
AC   ABH35428;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 235405 for detecting SNP TSC0057464.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
```

XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 235405; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 31.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 TGTACAGGGAGT 23
|| |||||||
Db 1 TTTAAAGGGAGT 12

RESULT 291
ABH43779
ID ABH43779 standard; DNA; 13 BP.
XX
AC ABH43779;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 243756 for detecting SNP TSC0059467.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75..
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 243756; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 7 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 31.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CCCTACGTGTAC 16
||| |||| |||
Db 1 CCCCACGTCTAC 12

RESULT 292
ABC60701/c
ID ABC60701 standard; DNA; 13 BP.
XX
AC ABC60701;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 60718 for detecting SNP TSC0016198.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 60718; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The

```
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 8 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
               |||| | |||||
Db         13 GTGTTCGGGGAG 2


RESULT 293
ABC62968
ID   ABC62968 standard; DNA; 13 BP.
XX
AC   ABC62968;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 62985 for detecting SNP TSC0016657.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 62985; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 1 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGA 21
              |||||| ||| |
Db          1 CGTGTAGAGGTA 12


RESULT 294
ABF21571/c
ID   ABF21571 standard; DNA; 13 BP.
XX
AC   ABF21571;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 121568 for detecting SNP TSC0030367.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 121568; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
              |||| || ||||
Db         13 TGTATAGAGAGT 2


RESULT 295
ABF36728
ID   ABF36728 standard; DNA; 13 BP.
XX
AC   ABF36728;
```

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XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 136725 for detecting SNP TSC0034175.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 136725; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 0 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity  83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
              |||| | |||||
Db          1 TGTAAATGGAGT 12


RESULT 296
ABH13931
ID   ABH13931 standard; DNA; 13 BP.
XX
AC   ABH13931;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 213908 for detecting SNP TSC0052066.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 213908; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity  83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              ||||||| | ||
Db          2 CCTACGTTTCCA 13


RESULT 297
ABC57872
ID   ABC57872 standard; DNA; 13 BP.
XX
AC   ABC57872;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 57889 for detecting SNP TSC0015568.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
```

```
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 57889; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              |||||||| | ||
Db          1 TACGTGTAGATG 12


RESULT 298
ABC11971/c
ID   ABC11971 standard; DNA; 13 BP.
XX
AC   ABC11971;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 11978 for detecting SNP TSC0002871.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 11978; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 7 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTCCAGG 28
              |||||||  |||
Db         12 AGGGAGTGTAGG 1


RESULT 299
ABH13930/c
ID   ABH13930 standard; DNA; 13 BP.
XX
AC   ABH13930;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 213907 for detecting SNP TSC0052066.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 213907; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 1 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              ||||||| | ||
```

```
Db         12 CCTACGTTTCCA 1


RESULT 300
ABH65565/c
ID   ABH65565 standard; DNA; 13 BP.
XX
AC   ABH65565;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 265542 for detecting SNP TSC0064360.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 265542; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 6 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              || ||||| |||
Db         12 TATGTGTATAGG 1


RESULT 301
ABF20036/c
ID   ABF20036 standard; DNA; 13 BP.
XX
AC   ABF20036;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 120033 for detecting SNP TSC0029958.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 120033; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 6 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              ||||| | ||||
Db         13 CCTACTTTTACA 2


RESULT 302
ABH30568
ID   ABH30568 standard; DNA; 13 BP.
XX
AC   ABH30568;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 230545 for detecting SNP TSC0056234.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
```

```
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 230545; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 1 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              |||||||| | |
Db          2 TACGTGTATATG 13


RESULT 303
ABF60517/c
ID   ABF60517 standard; DNA; 13 BP.
XX
AC   ABF60517;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 160514 for detecting SNP TSC0040412.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 160514; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 5 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
              ||||| | ||||
Db         12 GTGTAAAAGGAG 1


RESULT 304
ABH64063
ID   ABH64063 standard; DNA; 13 BP.
XX
AC   ABH64063;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 264040 for detecting SNP TSC0005398.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 264040; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
```

```
SQ   Sequence 13 BP; 6 A; 4 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              ||||||| |||
Db          2 CCTACGTAAACA 13


RESULT 305
ABC50869/c
ID   ABC50869 standard; DNA; 13 BP.
XX
AC   ABC50869;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 50886 for detecting SNP TSC0014248.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 50886; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 6 A; 5 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAGT 23
               ||| |||||||
Db          13 TGTTTAGGGAGT 2


RESULT 306
ABC59501/c
ID   ABC59501 standard; DNA; 13 BP.
XX
AC   ABC59501;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 59518 for detecting SNP TSC0015944.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 59518; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 4 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAGT 23
               | || |||||||
Db          13 TATAAAGGGAGT 2


RESULT 307
ABF97837
ID   ABF97837 standard; DNA; 13 BP.
XX
AC   ABF97837;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 197834 for detecting SNP TSC0048686.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
```

```
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 197834; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 5 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTAC 16
              | ||||||| |||
Db          2 CTCTACGTCTAC 13


RESULT 308
ABH35429/c
ID   ABH35429 standard; DNA; 13 BP.
XX
AC   ABH35429;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 235406 for detecting SNP TSC0057464.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 235406; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAGT 23
               | || |||||||
Db          13 TTTAAAGGGAGT 2


RESULT 309
ABF87829/c
ID   ABF87829 standard; DNA; 13 BP.
XX
AC   ABF87829;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 187826 for detecting SNP TSC0001439.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 187826; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
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CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 7 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity  83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          11 GTGTACAGGGAG 22
               ||||  ||||||
Db          12 GTGTCGAGGGAG 1


RESULT 310
ABC50868
ID   ABC50868 standard; DNA; 13 BP.
XX
AC   ABC50868;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 50885 for detecting SNP TSC0014248.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 50885; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 0 C; 5 G; 6 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity  83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAGT 23
               |||  |||||||
Db           1 TGTTTAGGGAGT 12


RESULT 311
ABF74653
ID   ABF74653 standard; DNA; 13 BP.
XX
AC   ABF74653;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 174650 for detecting SNP TSC0009116.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 174650; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity  83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           5 CCCTACGTGTAC 16
               ||||||||  ||
Db           1 CCCTACGTAAAC 12


RESULT 312
ABH30569/c
ID   ABH30569 standard; DNA; 13 BP.
XX
AC   ABH30569;
XX
DT   22-FEB-2002  (first entry)
```

```
XX
DE   Oligonucleotide SEQ ID NO 230546 for detecting SNP TSC0056234.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 230546; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              |||||||| | |
Db         12 TACGTGTATATG 1


RESULT 313
ABF89998
ID   ABF89998 standard; DNA; 13 BP.
XX
AC   ABF89998;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 189995 for detecting SNP TSC0046736.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 189995; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 0 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAGT 23
               | || |||||||
Db           1 TATATAGGGAGT 12


RESULT 314
ABC43390
ID   ABC43390 standard; DNA; 13 BP.
XX
AC   ABC43390;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 43407 for detecting SNP TSC0012844.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
```

```
XX
PS   Claim 1; SEQ ID NO 43407; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
               |||| ||||| |
Db          1 TGTAGAGGGAAT 12


RESULT 315
ABC43391/c
ID   ABC43391 standard; DNA; 13 BP.
XX
AC   ABC43391;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 43408 for detecting SNP TSC0012844.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 43408; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
               |||| ||||| |
Db          1 TGTAGAGGGAAT 12


RESULT 316
ABC60699/c
ID   ABC60699 standard; DNA; 13 BP.
XX
AC   ABC60699;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 60716 for detecting SNP TSC0016198.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 60716; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 7 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
               ||||  ||||||
Db         13 GTGTTTAGGGAG 2
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```
RESULT 317
ABC37804
ID   ABC37804 standard; DNA; 13 BP.
XX
AC   ABC37804;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 37821 for detecting SNP TSC0011747.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 37821; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match            31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity  83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
              | || |||||||
Db          1 TTTAGAGGGAGT 12


RESULT 318
ABF40374/c
ID   ABF40374 standard; DNA; 13 BP.
XX
AC   ABF40374;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 140371 for detecting SNP TSC0035182.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 140371; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match            31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity  83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTAC 16
              |||||||| | |
Db         12 CCCTACGTATCC 1


RESULT 319
ABH37109
ID   ABH37109 standard; DNA; 13 BP.
XX
AC   ABH37109;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 237086 for detecting SNP TSC0057833.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
```

```
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 237086; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 6 A; 4 C; 2 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              ||||||  ||||
Db          2 CCTACGAATACA 13


RESULT 320
ABC76136
ID   ABC76136 standard; DNA; 13 BP.
XX
AC   ABC76136;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 76153 for detecting SNP TSC0019495.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 76153; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              | ||||||  |||
Db          2 TGCGTGTAAAGG 13


RESULT 321
ABC05017
ID   ABC05017 standard; DNA; 13 BP.
XX
AC   ABC05017;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 5008 for detecting SNP TSC0001738.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 5008; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 6 C; 1 G; 3 T; 0 U; 0 Other;
```

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  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTAC 16
              ||||||| |||
Db          2 CCCTACGATTAC 13


RESULT 322
ABC60700
ID   ABC60700 standard; DNA; 13 BP.
XX
AC   ABC60700;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 60717 for detecting SNP TSC0016198.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 60717; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 1 A; 1 C; 8 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
              |||| | |||||
Db          1 GTGTTCGGGGAG 12


RESULT 323
ABF20037
ID   ABF20037 standard; DNA; 13 BP.
XX
AC   ABF20037;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 120034 for detecting SNP TSC0029958.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 120034; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTACA 17
              ||||| | ||||
Db          1 CCTACTTTTACA 12


RESULT 324
ABH30583/c
ID   ABH30583 standard; DNA; 13 BP.
XX
AC   ABH30583;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 230560 for detecting SNP TSC0056234.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
```

```
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 230560; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              |||||||| | |
Db         12 TACGTGTATACG 1


RESULT 325
ABF60518
ID   ABF60518 standard; DNA; 13 BP.
XX
AC   ABF60518;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 160515 for detecting SNP TSC0040412.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 160515; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGGAG 22
              ||||| | ||||
Db          2 GTGTAGAAGGAG 13


RESULT 326
ABH43778/c
ID   ABH43778 standard; DNA; 13 BP.
XX
AC   ABH43778;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 243755 for detecting SNP TSC0059467.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 243755; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
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```
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 1 C; 7 G; 2 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity  83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTAC 16
              ||| |||| |||
Db         13 CCCCACGTCTAC 2


RESULT 327
ABH65564
ID   ABH65564 standard; DNA; 13 BP.
XX
AC   ABH65564;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 265541 for detecting SNP TSC0064360.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 265541; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity  83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              || ||||| |||
Db          2 TATGTGTATAGG 13


RESULT 328
ABC56487
ID   ABC56487 standard; DNA; 13 BP.
XX
AC   ABC56487;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 56504 for detecting SNP TSC0015314.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 56504; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity  83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CCCTACGTGTAC 16
              | ||||| |||
Db          1 CACTACGTTTAC 12


RESULT 329
ABC85927/c
ID   ABC85927 standard; DNA; 13 BP.
XX
AC   ABC85927;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 85944 for detecting SNP TSC0021600.
```

```
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 85944; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAGT 23
               |||| |||| ||
Db          13 TGTAAAGGGTGT 2


RESULT 330
ABC37720
ID   ABC37720 standard; DNA; 13 BP.
XX
AC   ABC37720;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 37737 for detecting SNP TSC0011735.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 37737; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match           31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACAGG 19
              ||||| || |||
Db          2 TACGTATATAGG 13


RESULT 331
ABC64859/c
ID   ABC64859 standard; DNA; 13 BP.
XX
AC   ABC64859;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 64876 for detecting SNP TSC0017093.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 64876; 29pp + Sequence Listing; German.
```

```
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 8 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          11 GTGTACAGGGAG 22
               | ||| ||||||
Db          12 GGGTATAGGGAG 1


RESULT 332
ABF82919
ID   ABF82919 standard; DNA; 13 BP.
XX
AC   ABF82919;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 182916 for detecting SNP TSC0045193.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 182916; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 6 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           6 CCTACGTGTACA 17
               ||||| | ||||
Db           1 CCTACATATACA 12


RESULT 333
ABF59323/c
ID   ABF59323 standard; DNA; 13 BP.
XX
AC   ABF59323;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 159320 for detecting SNP TSC0040109.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 159320; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGAGT 23
               | || ||||||||
Db          13 TTTATAGGGAGT 2


RESULT 334
```

```
ABF87827/c
ID   ABF87827 standard; DNA; 13 BP.
XX
AC   ABF87827;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 187824 for detecting SNP TSC0001439.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 187824; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          11 GTGTACAGGGAG 22
               ||||  ||||||
Db          12 GTGTTAAGGGAG 1


RESULT 335
ABF87828
ID   ABF87828 standard; DNA; 13 BP.
XX
AC   ABF87828;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 187825 for detecting SNP TSC0001439.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 187825; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 1 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          11 GTGTACAGGGAG 22
               ||||  ||||||
Db           2 GTGTCGAGGGAG 13


RESULT 336
ABZ72790
ID   ABZ72790 standard; RNA; 13 BP.
XX
AC   ABZ72790;
XX
DT   09-APR-2003  (first entry)
XX
DE   Rod opsin hammerhead ribozyme target oligonucleotide SEQ ID NO:30.
XX
KW   Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
KW   ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KW   diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KW   blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX
OS   Homo sapiens.
XX
PN   WO200288320-A2.
XX
PD   07-NOV-2002.
XX
PF   01-MAY-2002; 2002WO-US013679.
XX
PR   01-MAY-2001; 2001US-00847601.
XX
PA   (UYFL ) UNIV FLORIDA.
XX
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```
PI   Lewin AS,  Shaw LC,  Grant MB;
XX
DR   WPI; 2003-111880/10.
XX
PT   A recombinant adeno-associated virus-vectored ribozyme composition,
PT   useful for treating a disease or dysfunction of the mammalian eye e.g.
PT   retinal disease, e.g. diabetic retinopathy or age-related macular
PT   degeneration.
XX
PS   Claim 1; Page 67; 115pp; English.
XX
CC   The present invention describes a recombinant adeno-associated virus
CC   (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
CC   first ribozyme that specifically cleaves an mRNA encoding a protein,
CC   polypeptide, or peptide selected from the group of rod opsin, iNOS,
CC   RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
CC   alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC   vector comprising a polynucleotide encoding the ribozyme, where the
CC   polynucleotide operably positioned downstream of at least a first
CC   promoter that directs expression of the polynucleotide in a selected
CC   mammalian cell transformed with the vector; (c) a viral particle
CC   comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC   comprising the ribozyme or the polynucleotide; or (e) a host cell
CC   comprising the ribozyme or the polynucleotide. Also described is a method
CC   for decreasing the amount of mRNA encoding a selected polypeptide in a
CC   retinal cell of a mammalian eye, comprising providing to the eye the
CC   composition described above, and for a time effective to specifically
CC   cleave the mRNA in the cell. (I) has ophthalmological activity, and can
CC   be used in gene therapy. (I) can be used for treating a disease or
CC   dysfunction of the mammalian eye, such as a retinal disease or retinal
CC   dysfunction, (diabetic) retinopathy, or (age-related) macular
CC   degeneration. (I) is also useful for manufacturing a medicament for
CC   treating the diseases mentioned above, including autosomal dominant
CC   retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
CC   for treating, decreasing the severity, or ameliorating the symptoms of a
CC   pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC   blindness, a reduction in central or peripheral vision, or a reduction in
CC   total vision. ABZ72763 to ABZ72953 represent sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 13 BP; 2 A; 5 C; 3 G; 0 T; 3 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   66.7%;  Pred. No. 2.3e+02;
  Matches    8;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCTACGT 12
              | ||| |:|||:
Db          1 CAGGCUCUACGU 12


RESULT 337
ADD50029
ID   ADD50029 standard; DNA; 13 BP.
XX
AC   ADD50029;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Specific nucleic acid binding agent 13m.
XX
KW   nucleic acid hybridisation; specific nucleic acid binding agent; SNABA;
KW   high throughput screening; microarray; ss; probe.
XX
OS   Synthetic.
XX
PN   US2003180729-A1.
XX
PD   25-SEP-2003.
XX
PF   22-MAR-2002; 2002US-00104307.
XX
PR   22-MAR-2002; 2002US-00104307.
XX
PA   (GENO-) GENOMETRIX GENOMICS INC.
XX
PI   Gunning KB,  Powdrill T,  Hogan M;
XX
DR   WPI; 2003-843930/78.
XX
PT   Hybridizing a nucleic acid and a specific nucleic acid binding agent uses
PT   a polycationizable attractor compound giving increased hybridization rate
PT   and is useful in high throughput screening microarray techniques.
XX
PS   Example 4; SEQ ID NO 26; 31pp; English.
XX
CC   The invention relates to a method of hybridising a nucleic acid and a
CC   specific nucleic acid binding agent (SNABA). The invention is useful in
CC   high throughput screening microarray techniques. The hybridisation rate
CC   is increased compared to conventional microarray techniques. The present
CC   sequence represents a specific nucleic acid binding agent (SNABA).
XX
SQ   Sequence 13 BP; 2 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             31.4%;  Score 8.8;  DB 1;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGAGT 23
              |||| |||| ||
Db          2 TGTAGAGGGCGT 13


RESULT 338
ABC35484/c
ID   ABC35484 standard; DNA; 13 BP.
XX
AC   ABC35484;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 35501 for detecting SNP TSC0011237.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 35501; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
```

```
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 1 Other;

  Query Match             30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGT 12
              :|||||||||
Db         13 RCCCTACGT 5


RESULT 339
ABF27735
ID   ABF27735 standard; DNA; 13 BP.
XX
AC   ABF27735;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 127732 for detecting SNP TSC0031982.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 127732; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 6 C; 1 G; 2 T; 0 U; 1 Other;

  Query Match             30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGT 12
              :|||||||||
Db         1 RCCCTACGT 9


RESULT 340
ABC01632/c
ID   ABC01632 standard; DNA; 13 BP.
XX
AC   ABC01632;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 1623 for detecting SNP TSC0000588.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 1623; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 1 C; 6 G; 1 T; 0 U; 1 Other;

  Query Match             30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGT 12
              :|||||||||
Db         13 RCCCTACGT 5


RESULT 341
ABC09239/c
ID   ABC09239 standard; DNA; 13 BP.
XX
AC   ABC09239;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 9230 for detecting SNP TSC0002450.
```

```
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 9230; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 1 Other;

  Query Match             30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              |||||||||:
Db          9 TACGTGTAY 1


RESULT 342
ABF95262
ID   ABF95262 standard; DNA; 13 BP.
XX
AC   ABF95262;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 195259 for detecting SNP TSC0048038.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 195259; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 1 C; 2 G; 4 T; 0 U; 1 Other;

  Query Match             30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              |||||||||:
Db          5 TACGTGTAY 13


RESULT 343
ABF20736/c
ID   ABF20736 standard; DNA; 13 BP.
XX
AC   ABF20736;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 120733 for detecting SNP TSC0030127.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 120733; 29pp + Sequence Listing; German.
```

```
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 1 C; 5 G; 3 T; 0 U; 1 Other;

  Query Match             30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGT 12
              :||||||||
Db         13 RCCCTACGT 5


RESULT 344
ABC61865/c
ID   ABC61865 standard; DNA; 13 BP.
XX
AC   ABC61865;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 61882 for detecting SNP TSC0016441.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 61882; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 6 A; 2 C; 1 G; 3 T; 0 U; 1 Other;

  Query Match             30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              ||||||||:
Db          9 TACGTGTAY 1


RESULT 345
ABF95263/c
ID   ABF95263 standard; DNA; 13 BP.
XX
AC   ABF95263;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 195260 for detecting SNP TSC0048038.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 195260; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 2 C; 1 G; 5 T; 0 U; 1 Other;

  Query Match             30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              ||||||||:
Db          9 TACGTGTAY 1


RESULT 346
```

```
ABF84330/c
ID   ABF84330 standard; DNA; 13 BP.
XX
AC   ABF84330;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 184327 for detecting SNP TSC0045489.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 184327; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 1 C; 6 G; 2 T; 0 U; 1 Other;

  Query Match             30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGT 12
              :|||||||| .
Db         13 RCCCTACGT 5


RESULT 347
ABH01272
ID   ABH01272 standard; DNA; 13 BP.
XX
AC   ABH01272;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 201249 for detecting SNP TSC0049513.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 201249; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 1 C; 2 G; 6 T; 0 U; 1 Other;

  Query Match             30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              |||||||:
Db          5 TACGTGTAY 13


RESULT 348
ABH64362
ID   ABH64362 standard; DNA; 13 BP.
XX
AC   ABH64362;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 264339 for detecting SNP TSC0064059.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
```

```
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 264339; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 1 C; 3 G; 4 T; 0 U; 1 Other;

  Query Match             30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              ||||||||:
Db          5 TACGTGTAY 13


RESULT 349
ABH64363/c
ID   ABH64363 standard; DNA; 13 BP.
XX
AC   ABH64363;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 264340 for detecting SNP TSC0064059.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 264340; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 3 C; 1 G; 4 T; 0 U; 1 Other;

  Query Match             30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              ||||||||:
Db          9 TACGTGTAY 1


RESULT 350
ABC01633
ID   ABC01633 standard; DNA; 13 BP.
XX
AC   ABC01633;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 1624 for detecting SNP TSC0000588.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 1624; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 1 A; 6 C; 1 G; 4 T; 0 U; 1 Other;

  Query Match             30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
```

```
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGT 12
              :|||||||||
Db          1 RCCCTACGT 9


RESULT 351
ABC61864
ID   ABC61864 standard; DNA; 13 BP.
XX
AC   ABC61864;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 61881 for detecting SNP TSC0016441.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 61881; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 1 C; 2 G; 6 T; 0 U; 1 Other;

  Query Match           30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              ||||||||:
Db          5 TACGTGTAY 13


RESULT 352
ABF84331
ID   ABF84331 standard; DNA; 13 BP.
XX
AC   ABF84331;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 184328 for detecting SNP TSC0045489.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 184328; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 6 C; 1 G; 3 T; 0 U; 1 Other;

  Query Match           30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGT 12
              :|||||||||
Db          1 RCCCTACGT 9


RESULT 353
ABH01273/c
ID   ABH01273 standard; DNA; 13 BP.
XX
AC   ABH01273;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 201250 for detecting SNP TSC0049513.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
```

```
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 201250; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 6 A; 2 C; 1 G; 3 T; 0 U; 1 Other;

  Query Match             30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              ||||||||:
Db          9 TACGTGTAY 1


RESULT 354
ABC09238
ID   ABC09238 standard; DNA; 13 BP.
XX
AC   ABC09238;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 9229 for detecting SNP TSC0002450.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 9229; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 1 Other;

  Query Match             30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TACGTGTAC 16
              ||||||||:
Db          5 TACGTGTAY 13


RESULT 355
ABC35485
ID   ABC35485 standard; DNA; 13 BP.
XX
AC   ABC35485;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 35502 for detecting SNP TSC0011237.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 35502; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
```

```
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 4 C; 1 G; 2 T; 0 U; 1 Other;

  Query Match           30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGT 12
              :||||||||
Db          1 RCCCTACGT 9


RESULT 356
ABF27734/c
ID   ABF27734 standard; DNA; 13 BP.
XX
AC   ABF27734;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 127731 for detecting SNP TSC0031982.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 127731; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 1 Other;

  Query Match           30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGT 12
              :||||||||
Db         13 RCCCTACGT 5


RESULT 357
ABF20737
ID   ABF20737 standard; DNA; 13 BP.
XX
AC   ABF20737;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 120734 for detecting SNP TSC0030127.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 120734; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 5 C; 1 G; 3 T; 0 U; 1 Other;

  Query Match           30.7%;  Score 8.6;  DB 1;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGT 12
              :||||||||
Db          1 RCCCTACGT 9


RESULT 358
AAQ51822/c
ID   AAQ51822 standard; RNA; 10 BP.
XX
AC   AAQ51822;
XX
DT   25-MAR-2003  (revised)
DT   26-MAY-1994  (first entry)
XX
DE   mdr-1 mRNA ribozyme cleavable nucleotide NT612.
XX
```

```
KW   Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
KW   resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
KW   actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
KW   adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
KW   human; chronic myelogenous leukemia; CML; follicular lymphoma;
KW   B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
KW   neuroblastoma; lung cancer; genetic drift; mutation; ss.
XX
OS   Homo sapiens.
XX
PN   WO9323057-A1.
XX
PD   25-NOV-1993.
XX
PF   13-MAY-1993;   93WO-US004573.
XX
PR   14-MAY-1992;   92US-00882822.
PR   14-MAY-1992;   92US-00882885.
PR   26-AUG-1992;   92US-00936110.
PR   26-AUG-1992;   92US-00936421.
PR   26-AUG-1992;   92US-00936422.
PR   26-AUG-1992;   92US-00936531.
PR   26-AUG-1992;   92US-00936532.
PR   07-DEC-1992;   92US-00987131.
PR   19-JAN-1993;   93US-00006122.
PR   19-JAN-1993;   93US-00008910.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Draper KG;
XX
DR   WPI; 1993-386203/48.
XX
PT   New enzymatic RNA molecules (ribozymes) - which cleave mRNA associated
PT   with tumours or mRNA expressed from gene encoding multiple drug
PT   resistance.
XX
PS   Claim 3; Fig 2; 69pp; English.
XX
CC   The sequences given in AAQ51816-24 represent areas of the multiple drug
CC   resistance (mdr-1) mRNA which are accessible to the ribozyme of the
CC   invention. The mdr-1 gene encodes a 170 kD integral membrane protein
CC   which confers resistance to certain chemotherapeutic agents, such as
CC   colchicine, doxorubicin, actinomycin D and vinblastine. The gene is
CC   normally expressed in cells of the colon, small intestine, kidney, liver
CC   and adrenal gland. High levels of MDR1 transcript have been found in
CC   adenocarcinomas that are intrinsically resistant to a broad range of
CC   chemotherapeutic agents, such as those derived from adrenal, kidney,
CC   liver and bowel. The ribozymes of the invention may be used to inhibit
CC   the development or expression of a transformed phenotype in man and other
CC   animals by modulating expression of a gene that contributes to, or
CC   inhibits the expression of chronic myelogenous leukemia (CML),
CC   promyelocytic leukemia, follicular lymphoma, B-cell acute lymphocytic
CC   leukemia, breast cancer, colon carcinoma, neuroblastoma, lung cancer, and
CC   other neoplastic conditions. Cleavage of target mRNAs expressed in pre-
CC   neoplastic and transformed cells elicits inhibition of the transformed
CC   state. mdr-1 specific ribozymes remove the mechanism of drug resistance
CC   used by transformed cells and thus enhances drug therapies for tumours.
CC   The ribozymes may also be used to study genetic drift and mutations
CC   within cells. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 10 BP; 1 A; 4 C; 2 G; 0 T; 3 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              || |||||||
Db         10 GGAAGTCCAG 1


RESULT 359
AAV48046/c
ID   AAV48046 standard; DNA; 10 BP.
XX
AC   AAV48046;
XX
DT   19-OCT-1998  (first entry)
XX
DE   Human B7-2 targetted oligonucleotide 10991.
XX
KW   ss; human; B7; T cell; inflammation; autoimmune disease; cell activation;
KW   cell proliferation.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .10
FT                   /*tag=  a
FT                   /note= "Phosphorothioate linkages"
XX
PN   WO9829124-A1.
XX
PD   09-JUL-1998.
XX
PF   16-DEC-1997;   97WO-US023270.
XX
PR   31-DEC-1996;   96US-00777266.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Vickers TA;
XX
DR   WPI; 1998-387783/33.
XX
PT   New oligo:nucleotide(s) that modulate expression of B7 proteins - used
PT   for, e.g. controlling activation and proliferation of T cells,
PT   particularly for treatment, diagnosis and prevention of inflammation.
XX
PS   Example 1; Page 39; 120pp; English.
XX
CC   The oligonucleotides which specifically hybridise to B7 modulate its
CC   expression (and thus T cell activation and proliferation). This is
CC   particularly useful for treatment and prevention of inflammation and
CC   autoimmune diseases, e.g. asthma, (juvenile) diabetes, myasthenia gravis,
CC   Grave's disease, rheumatoid arthritis, allograft rejection, psoriasis,
CC   (systemic) lupus erythematosus, multiple sclerosis, contact dermatitis,
CC   rhinitis, allergy, cancer and metastases. The oligonucleotides may also
CC   be used to manipulate T cell activation ex vivo; to determine or detect
CC   B7 protein expression; for diagnosis; as assay and purification reagents,
CC   and to study physiological roles of B7 proteins
XX
SQ   Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAG 22
              |||| |||||
Db         10 GTACGGGGAG 1


RESULT 360
AAZ84063
ID   AAZ84063 standard; DNA; 10 BP.
XX
AC   AAZ84063;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #3297.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
```

```
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 147; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGT 23
              |||||| |||
Db          1 TACAGGAAGT 10


RESULT 361
AAZ84365/c
ID   AAZ84365 standard; DNA; 10 BP.
XX
AC   AAZ84365;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #3599.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 155; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 6 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGG 20
              |||||| |||
Db         10 GTGTACGGGG 1


RESULT 362
AAZ84677
ID   AAZ84677 standard; DNA; 10 BP.
XX
AC   AAZ84677;
XX
DT   07-APR-2000  (first entry)
```

```
XX
DE   Metastatic breast tumour cell downregulated transcript tag #3911.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 163; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAG 22
              || |||||||
Db          1 GTGCAGGGAG 10


RESULT 363
AAZ81464/c
ID   AAZ81464 standard; DNA; 10 BP.
XX
AC   AAZ81464;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #698.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 77; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAG 22
              |||||||| |
Db         10 GTACAGGGTG 1


RESULT 364
AAZ83955
ID   AAZ83955 standard; DNA; 10 BP.
```

```
XX
AC   AAZ83955;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #3189.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 144; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCTAC 10
              | ||||||||
Db          1 CCGGCCCTAC 10


RESULT 365
```

```
AAZ84972/c
ID   AAZ84972 standard; DNA; 10 BP.
XX
AC   AAZ84972;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #4206.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 171; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAGTC 24
              |||| |||||
Db         10 ACAGAGAGTC 1
```

```
RESULT 366
AAZ85775/c
ID   AAZ85775 standard; DNA; 10 BP.
XX
AC   AAZ85775;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #5009.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 192; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 3 A; 4 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGA 21
               ||||| ||||
Db          10 TGTACTGGGA 1


RESULT 367
AAZ82697
ID   AAZ82697 standard; DNA; 10 BP.
XX
AC   AAZ82697;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1931.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 111; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          19 GGAGTCCAGG 28
               |||| |||||
Db           1 GGAGCCCAGG 10
```

```
RESULT 368
AAZ79793
ID   AAZ79793 standard; DNA; 10 BP.
XX
AC   AAZ79793;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human cystic kidney cell upregulated gene SAGE tag, SEQ ID NO:84.
XX
KW   SAGE tag; serial analysis of gene expression; diagnosis;
KW   differential gene expression; characterisation; targetted expression;
KW   tumour; cancer; immunotherapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO9966303-A2.
XX
PD   23-DEC-1999.
XX
PF   17-JUN-1999;  99WO-US013820.
XX
PR   19-JUN-1998;  98US-0089833P.
PR   19-JUN-1998;  98US-0089844P.
PR   19-JUN-1998;  98US-0089853P.
PR   19-JUN-1998;  98US-0089878P.
PR   19-JUN-1998;  98US-0089991P.
PR   19-JUN-1998;  98US-0089992P.
PR   19-JUN-1998;  98US-0089993P.
PR   19-JUN-1998;  98US-0089994P.
PR   19-JUN-1998;  98US-0089997P.
PR   19-JUN-1998;  98US-0089999P.
PR   19-JUN-1998;  98US-0090000P.
PR   19-JUN-1998;  98US-0090035P.
PR   19-JUN-1998;  98US-0090036P.
PR   19-JUN-1998;  98US-0090039P.
PR   19-JUN-1998;  98US-0090040P.
PR   19-JUN-1998;  98US-0090041P.
PR   19-JUN-1998;  98US-0090042P.
PR   19-JUN-1998;  98US-0090043P.
PR   19-JUN-1998;  98US-0090044P.
PR   19-JUN-1998;  98US-0090045P.
PR   19-JUN-1998;  98US-0090047P.
PR   19-JUN-1998;  98US-0090048P.
PR   19-JUN-1998;  98US-0090072P.
PR   19-JUN-1998;  98US-0090076P.
PR   19-JUN-1998;  98US-0090077P.
PR   19-JUN-1998;  98US-0090078P.
PR   19-JUN-1998;  98US-0090079P.
PR   19-JUN-1998;  98US-0090080P.
PR   08-DEC-1998;  98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106132/09.
XX
PT   New polynucleotide useful in cancer immunotherapy.
XX
PS   Claim 1; Page 56; 97pp; English.
XX
CC   Sequences AAZ79710-Z79916 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts which are
CC   differentially expressed in a variety of normal or malignant cell types.
CC   Some of the transcripts correspond to known genes or ESTs (expressed
CC   sequence tags) which were previously unknown to be preferentially or
CC   differentially expressed in that particular cell type, while other
CC   transcripts correspond to novel genes. The invention also provides a
CC   nucleotide comprising a promoter sequence derived from one of the
CC   differentially expressed genes, which may optionally be operably linked
CC   to a foreign nucleotide sequence, and gene delivery vehicles and host
CC   cells comprising the polynucleotides of the invention. A nucleotide
CC   comprising sequences AAZ79710-Z79916 may be used in diagnostic procedures
CC   to characterise a cell of a specific tissue type and to determine whether
CC   it is normal or malignant. They may be used to screen for agents that
CC   modulate expression of differentially expressed genes compound. The
CC   promoter/foreign gene construct of the invention may be used for
CC   targetted expression of the foreign gene in a particular cell type. For
CC   example, a promoter derived from a gene preferentially expressed in
CC   dendritic cells (antigen-presenting cells, or APCs), may be operably
CC   linked to a sequence encoding an immunostimulatory molecule and a
CC   sequence encoding an antigen. Such a construct could be transduced into
CC   APCs and would be useful for inducing an immune response by educating
CC   immune effector cells in vivo, or in cancer immunotherapy
XX
SQ   Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCTAC 10
              | |||||||||
Db          1 CCGGCCCTAC 10
```

```
RESULT 369
AAF32888/c
ID   AAF32888 standard; DNA; 10 BP.
XX
AC   AAF32888;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Human B7-2 mRNA antisense oligonucleotide SEQ ID NO: 85.
XX
KW   Human; mouse; B7-1; B7-2; antisense; PCR primer; inflammation;
KW   autoimmune disorder; phosphorothioate backbone; ss.
XX
OS   Homo sapiens.
XX
PN   WO200074687-A1.
XX
PD   14-DEC-2000.
XX
PF   25-MAY-2000; 2000WO-US014471.
XX
PR   04-JUN-1999;   99US-00326186.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Vickers TA,  Karras JG;
XX
DR   WPI; 2001-049991/06.
XX
PT   Novel compound for diagnosing, preventing and treating immune disorders,
PT   comprising an oligonucleotide that specifically hybridizes with a nucleic
PT   acid sequence encoding B7 protein.
XX
PS   Example 1; Page 51; 162pp; English.
XX
CC   The present invention provides sequences of antisense oligonucleotides
CC   targeted at the murine and human B7-1 and B7-2 coding and mRNA sequences.
CC   The antisense sequences have phosphorothioate backbones and some
CC   nucleotides are 2'-methoxyethoxy residues. The sequences can be used in
CC   the treatment of inflammatory and autoimmune disorders, including asthma,
CC   juvenile diabetes mellitus, myasthenia gravis, Graves' disease,
CC   rheumatoid arthritis, allograft rejection, inflammatory bowel disease,
```

```
CC   multiple sclerosis, psoriasis, systemic lupus erythematosus, contact
CC   dermatitis, rhinitis, allergies and cancer
XX
SQ   Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAG 22
              |||| |||||
Db         10 GTACGGGGAG 1


RESULT 370
AAH20000/c
ID   AAH20000 standard; DNA; 10 BP.
XX
AC   AAH20000;
XX
DT   07-AUG-2001  (first entry)
XX
DE   Mouse Treg immunoregulatory network related tag #71.
XX
KW   Mouse; EST; expressed sequence tag; contig; immunoregulation;
KW   immunosuppression; Treg immunoregulatory network; inflammatory;
KW   immune disorder; T regulatory lymphocyte; T helper cell; dermatological;
KW   antiinflammatory; immunosuppressive; antiarteriosclerotic; antiallergic;
KW   antidiabetic; neuroprotective; osteopathic; antiarthritic; anti-ulcer;
KW   rheumatoid arthritis; osteoarthritis; glomerular nephritis; diabetes;
KW   inflammatory bowel disease; vascular disease; atherosclerosis; psoriasis;
KW   vasculitis; skin disease; dermatitis; Crohn's disease; lung disease;
KW   ulcerative colitis; lupus erythematosus; autoimmune disorder; emphysema;
KW   hypersensitivity; multiple sclerosis; chronic bronchitis; asthma;
KW   idiopathic pulmonary fibrosis; primer; probe; tag; ss.
XX
OS   Mus musculus.
OS   Synthetic.
XX
PN   WO200127267-A2.
XX
PD   19-APR-2001.
XX
PF   06-OCT-2000; 2000WO-GB003821.
XX
PR   08-OCT-1999;   99GB-00023790.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
XX
PI   Adams E,  Waldmann H,  Cobbold S,  Zelenika D;
XX
DR   WPI; 2001-300216/31.
XX
PT   Isolated genes differentially expressed in T helper 1 (Th1) and 2 (Th2)
PT   and T regulatory (Treg) lymphocytes useful in prophylaxis, diagnosis and
PT   therapy of inflammatory and immune diseases.
XX
PS   Example 4; Page 5; 29pp; English.
XX
CC   The present invention describes an isolated gene (I) obtainable by: (a)
CC   comparing the expression of one or more genes in populations of T helper
CC   1 lymphocytes (Th1)-, Th2- and T regulatory cells (Treg)-enriched cell
CC   populations to identify a gene which is differentially expressed in the
CC   populations; and (b) isolating the gene. (I) can have dermatological,
CC   antiinflammatory, immunosuppressive, antiarteriosclerotic, antiallergic,
CC   antidiabetic, neuroprotective, osteopathic, antiarthritic and anti-ulcer
CC   activities. (I) can be used in anti-inflammatory and immunoregulatory
CC   compositions for use in therapy, prophylaxis, or diagnosis and/or in a
CC   pharmaceutical excipient, a unit dosage form or in a form suitable for
CC   local or systemic administration. Methods from the present invention can
CC   be used for detecting Th1 and/or Th2 and/or Treg cells in a biological
CC   sample, for cell typing or for determining the number of Th1 and/or Th2
CC   and/or Treg cells in a biological sample. Diseases which may be treated
CC   by compositions of the invention include rheumatoid and osteoarthritis,
CC   glomerular nephritis, diabetes, inflammatory bowel disease, vascular
CC   diseases e.g. atherosclerosis and vasculitis, skin diseases such as
CC   psoriasis and dermatitis, Crohn's disease, ulcerative colitis, lupus
CC   erythematosus, autoimmune disorders, hypersensitivity, multiple
CC   sclerosis, and lung diseases e.g. chronic bronchitis, emphysema,
CC   idiopathic pulmonary fibrosis and asthma. (I) can also be used as markers
CC   for analysis of serum, urine and biopsy, particularly during and after
CC   therapy for multiple sclerosis. AAH19930 to AAH20034 and AAB75133
CC   represent sequence used in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGA 21
              ||||| ||||
Db         10 TGTACGGGGA 1


RESULT 371
AAH64417/c
ID   AAH64417 standard; cDNA; 10 BP.
XX
AC   AAH64417;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1257.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US031922.
XX
PR   24-NOV-1999;   99US-00448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell type,
PT   such as cancer cell, comprises transcriptomes expressed in particular
PT   cell types.
XX
PS   Claim 11; Page 68; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences AAH63161-
CC   AAH64724 is expressed by the cell. The transcriptomes described in the
CC   invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of the
CC   transcriptomes described in the exemplification of the invention
XX
SQ   Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGA 21
```

```
              |||||||||
Db         10 TGTACGGGGA 1


RESULT 372
ABA06027/c
ID   ABA06027 standard; cDNA; 10 BP.
XX
AC   ABA06027;
XX
DT   10-JAN-2002  (first entry)
XX
DE   Human normal hepatocyte expression gene cDNA, SEQ ID NO: 4.
XX
KW   Human; hepatocyte; gene expression; hepatopathy; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001211883-A.
XX
PD   07-AUG-2001.
XX
PF   31-JAN-2000; 2000JP-00023170.
XX
PR   31-JAN-2000; 2000JP-00023170.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2001-629566/73.
XX
PT   Human normal hepatocyte expression gene group.
XX
PS   Claim 1; Page 6; 26pp; Japanese.
XX
CC   The invention relates to a human normal hepatocyte expression gene group
CC   comprising 200 genes in the human normal hepatocyte. The cDNA of each
CC   gene comprises one of 200 fully defined nucleotide sequences as given in
CC   the specification. The gene group and the cDNAs corresponding to each of
CC   the genes in the group are useful in the diagnosis and treatment of human
CC   hepatopathy. The present sequence is a cDNA corresponding to a gene
CC   expressed by normal human hepatocytes
XX
SQ   Sequence 10 BP; 0 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              ||||| ||||
Db         10 GGGAGGCCAG 1


RESULT 373
AAF40935/c
ID   AAF40935 standard; DNA; 10 BP.
XX
AC   AAF40935;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7674.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 274; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 6 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGG 20
              |||||| |||
Db         10 GTGTACGGGG 1


RESULT 374
AAF40704
ID   AAF40704 standard; DNA; 10 BP.
XX
AC   AAF40704;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7443.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
```

PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 265; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCTACGTGTA 15
|||||||||
Db 1 CATACGTGTA 10

RESULT 375
AAF43233/c
ID AAF43233 standard; DNA; 10 BP.
XX
AC AAF43233;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11372.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 356; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 17 AGGGAGTCCA 26
||||| ||||
Db 10 AGGGACTCCA 1

RESULT 376
AAD25443
ID AAD25443 standard; DNA; 10 BP.
XX
AC AAD25443;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human GNRH2 gene polymorphism detecting primer #14.
XX
KW Human; gonadotropin-releasing hormone 2; GNRH2 gene; haplotyping;

```
KW   genotyping; gene therapy; reproductive disorder; polymorphism; primer;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO200187910-A2.
XX
PD   22-NOV-2001.
XX
PF   18-MAY-2001; 2001WO-US016353.
XX
PR   18-MAY-2000; 2000US-0205187P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Duda A,  Kliem SE,  Nandabalan K,  Sausker EA;
XX
DR   WPI; 2002-055683/07.
XX
PT   New genetic variants of gonadotropin-releasing hormone 2 isogene, useful
PT   in studying expression and function of protein and for screening drugs to
PT   treat diseases e.g. reproduction disorders.
XX
PS   Claim 18; Page 13; 64pp; English.
XX
CC   The invention relates to genetic variants of human gonadotropin-
CC   releasing hormone 2 (GNRH2) gene. The invention also relates to
CC   compositions and methods for haplotyping and/or genotyping the GNRH2 gene
CC   in an individual. Polynucleotides of the invention are useful for
CC   studying the expression and function of GNRH2 and in expressing GNRH2
CC   proteins for use in screening candidate drugs to treat diseases related
CC   to GNRH2 activity. They are also used in gene therapy. The methods of the
CC   invention are useful in determining whether an individual has a haplotype
CC   or haplotype pairs. The haplotyping method is useful for improving the
CC   efficiency and reliability of several steps in the discovery and
CC   development of drugs for treating diseases associated with GNRH2
CC   activity, e.g., reproductive disorders. The present sequence is a primer
CC   used for detecting human GNRH2 gene polymorphisms
XX
SQ   Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGG 20
               |||| |||||
Db          1 GTGTCCAGGG 10


RESULT 377
ABL52206/c
ID   ABL52206 standard; DNA; 10 BP.
XX
AC   ABL52206;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Human PER1 preferred oligonucleotide primer SEQ ID NO:131.
XX
KW   Human; period (Drosophila) homologue 1; PER1; polymorphic variant;
KW   polymorphic site; genotyping; haplotyping; circadian rhythm regulation;
KW   single nucleotide polymorphism; SNP; gene; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200222650-A2.
XX
PD   21-MAR-2002.
XX
PF   13-SEP-2001; 2001WO-US028780.
XX
PR   13-SEP-2000; 2000US-0232468P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Duda A,  Kliem SE,  Koshy B;
XX
DR   WPI; 2002-393941/42.
XX
PT   Novel isolated human period Drosophila homolog 1 polynucleotide, useful
PT   for therapeutic purposes, for studying the expression and function of the
PT   polynucleotide, and for expressing the homolog.
XX
PS   Claim 19; Page 16; 162pp; English.
XX
CC   The present invention describes an isolated human period (Drosophila)
CC   homologue 1, (PER1) polynucleotide (I) comprising a sequence which is a
CC   polymorphic variant for a reference sequence (ABL52077) for the PER1 gene
CC   or its fragment, or a polymorphic variant of a reference sequence
CC   (ABL52078) for a PER1 cDNA or its fragment. The present invention also
CC   describes methods for genotyping and haplotyping the PER1 gene of an
CC   individual. (I) is useful in studying the expression and function of
CC   PER1, and in expressing PER1 protein for use in screening for candidate
CC   drugs to treat diseases related to PER1 activity. (I) is useful for
CC   therapeutic purposes. A recombinant non-human organism transformed or
CC   transfected with (I) can be used for studying expression of the PER1
CC   isogenes in vivo, for in vivo screening and testing of drugs targeted
CC   against PER1 protein, and for testing the efficacy of therapeutic agents
CC   and compounds for disorders associated with circadian rhythm regulation.
CC   The present sequence represents a preferred oligonucleotide primer for
CC   human PER1, which is used in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 6 C; 1 G; 1 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGG 20
               |||| |||||
Db         10 GTGTGCAGGG 1


RESULT 378
ABL52211/c
ID   ABL52211 standard; DNA; 10 BP.
XX
AC   ABL52211;
XX
DT   12-JUL-2002  (first entry)
XX
DE   Human PER1 preferred oligonucleotide primer SEQ ID NO:136.
XX
KW   Human; period (Drosophila) homologue 1; PER1; polymorphic variant;
KW   polymorphic site; genotyping; haplotyping; circadian rhythm regulation;
KW   single nucleotide polymorphism; SNP; gene; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200222650-A2.
XX
PD   21-MAR-2002.
XX
PF   13-SEP-2001; 2001WO-US028780.
XX
PR   13-SEP-2000; 2000US-0232468P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Duda A,  Kliem SE,  Koshy B;
XX
DR   WPI; 2002-393941/42.
XX
PT   Novel isolated human period Drosophila homolog 1 polynucleotide, useful
PT   for therapeutic purposes, for studying the expression and function of the
```

PT polynucleotide, and for expressing the homolog.
XX
PS Claim 19; Page 16; 162pp; English.
XX
CC The present invention describes an isolated human period (Drosophila)
CC homologue 1, (PER1) polynucleotide (I) comprising a sequence which is a
CC polymorphic variant for a reference sequence (ABL52077) for the PER1 gene
CC or its fragment, or a polymorphic variant of a reference sequence
CC (ABL52078) for a PER1 cDNA or its fragment. The present invention also
CC describes methods for genotyping and haplotyping the PER1 gene of an
CC individual. (I) is useful in studying the expression and function of
CC PER1, and in expressing PER1 protein for use in screening for candidate
CC drugs to treat diseases related to PER1 activity. (I) is useful for
CC therapeutic purposes. A recombinant non-human organism transformed or
CC transfected with (I) can be used for studying expression of the PER1
CC isogenes in vivo, for in vivo screening and testing of drugs targeted
CC against PER1 protein, and for testing the efficacy of therapeutic agents
CC and compounds for disorders associated with circadian rhythm regulation.
CC The present sequence represents a preferred oligonucleotide primer for
CC human PER1, which is used in the exemplification of the present invention
XX
SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 18 GGGAGTCCAG 27
||||| ||||
Db 10 GGGAGCCCAG 1

RESULT 379
AAS98842/c
ID AAS98842 standard; DNA; 10 BP.
XX
AC AAS98842;
XX
DT 26-MAR-2002 (first entry)
XX
DE Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #208.
XX
KW Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;
KW cytostatic; gene therapy; malignant histiocytosis; isogene;
KW myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;
KW genotype; human; allele specific oligonucleotide; ASO; primer;
KW primer extension; ss.
XX
OS Homo sapiens.
XX
PN WO200179225-A2.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US012044.
XX
PR 12-APR-2000; 2000US-0196411P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Choi JY, Koshy B;
XX
DR WPI; 2002-075058/10.
XX
PT Novel polymorphic variants of colony stimulating factor 1 receptor useful
PT in studying expression and function of the protein, useful for screening
PT candidate drugs to treat diseases e.g. inflammatory disorders.
XX
PS Claim 17; Page 17; 164pp; English.
XX
CC The invention describes a novel isolated polynucleotide (I) comprising a
CC sequence which is a polymorphic variant (PV) of a reference sequence for
CC colony stimulating factor 1 receptor (CSF1R) gene, found on The
CC polypeptide are useful for improving the discovery and development of
CC drugs for treating diseases associated with CSF1R activity, e.g.,
CC malignant histiocytosis, myeloid malignancies, and inflammatory disorders
CC and the haplotypes can be used to validate CSF1R as a candidate target
CC for treating a specific condition or disease predicted to be associated
CC with CSF1R activity. Genotyping the CSF1R gene of an individual can also
CC be used in developing diagnostic tests and therapeutic treatments. (I) is
CC useful in studying the expression and function of CSF1R, and in
CC expressing CSF1R protein for use in screening for candidate drugs to
CC treat diseases related to CSF1R activity and in studying the effect of
CC the variation on the biological activity of CSF1R as well as on the
CC binding affinity of candidate drugs targeting CSF1R. Antibodies are
CC useful in a variety of diagnostic and prognostic formats and therapeutic
CC methods. A transgenic animal is useful in studying expression of the
CC CSF1R isogenes in vivo, for in vivo screening and testing of drugs
CC targeted against CSF1R protein, and for testing the efficacy of
CC therapeutic agents and compounds. Allele specific oligonucleotides (ASO)
CC are useful as probes and primers, and for assaying a polymorphism in the
CC target region. Without requiring any a priori knowledge of the phenotypic
CC effect of any particular CSF1R or haplotype the invention provides a
CC method for identifying lead compounds that are more likely to show
CC efficacy in clinical trials. This sequence is a primer used to detect
CC CSF1R gene polymorphisms by primer extension, described in the method of
CC the invention
XX
SQ Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GTGTACAGGG 20
|||| |||||
Db 10 GTGTTCAGGG 1

RESULT 380
ABK17003
ID ABK17003 standard; DNA; 10 BP.
XX
AC ABK17003;
XX
DT 26-MAR-2002 (first entry)
XX
DE Pyridoxal (Pyridoxine, vitamin B6) Kinase (PDXK) primer #26.
XX
KW Pyridoxal kinase; pyridoxine; vitamin B6;
KW PDXK autoimmune polyglandular disease type 1; transgenic animal;
KW gene therapy; primer extension; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200190125-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US016909.
XX
PR 24-MAY-2000; 2000US-0206664P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Duda A, Koshy B;
XX
DR WPI; 2002-106169/14.
XX
PT Isolated human pyridoxal (pyridoxine, vitamin B6) kinase polyNts, useful
PT for therapeutic purposes, for studying the expression and function of the
PT polyNt, and for expressing pyridoxal protein.
XX
PS Claim 19; Page 14; 135pp; English.
XX
CC The invention describes an isolated human pyridoxal (pyridoxine, vitamin

```
CC   B6) kinase, (PDXK) polynucleotide. The polynucleotide is useful in
CC   studying the expression and function of PDXK, and in expressing PDXK
CC   protein for use in screening for candidate drugs to treat PDXK related
CC   diseases and for therapeutic purposes. A transgenic animal is useful for
CC   studying expression of the PDXK isogenes in vivo, for in vivo screening
CC   and testing of drugs targeted against PDXK protein, and for testing the
CC   efficacy of therapeutic agents and compounds for autoimmune polyglandular
CC   disease type 1. The polypeptide is useful for studying the effect of the
CC   variation on the biological activity of PDXK and the binding affinity of
CC   candidate drugs targeting PDXK for the treatment of autoimmune
CC   polyglandular disease type 1. Genotyping and haplotyping is useful for
CC   improving the efficacy and reliability of several steps in the discovery
CC   and development of drugs for treating diseases associated with PDXK
CC   activity, e.g., autoimmune polyglandular disease type 1, to validate PDXK
CC   as a candidate agent for treating a specific condition or disease
CC   predicted to be associated with PDXK activity, and in the design of
CC   clinical trials of candidate drugs. This sequence is one of 38 (see
CC   ABK16978-ABK17015) primers used for detecting PDXK gene polymorphisms by
CC   primer extension terminates, described in the method of the invention
XX
SQ   Sequence 10 BP; 3 A; 2 C; 5 G; 0 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAG 22
              | ||||||||
Db          1 GCACAGGGAG 10


RESULT 381
AAD26864/c
ID   AAD26864 standard; DNA; 10 BP.
XX
AC   AAD26864;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human GPR4 gene polymorphism detecting primer #5.
XX
KW   Human; G-protein coupled receptor 4; GPR4; haplotyping; polymorphism;
KW   allele-specific oligonucleotide; ASO; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200187904-A2.
XX
PD   22-NOV-2001.
XX
PF   09-MAY-2001; 2001WO-US015097.
XX
PR   17-MAY-2000; 2000US-0204928P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bentivegna SC,' Duda AE,  Kazemi A,  Koshy B;
XX
DR   WPI; 2002-097579/13.
XX
PT   Haplotyping, (H1), the G-protein coupled receptor 4 (GPR4) gene of an
PT   individual, comprising determining which haplotype an individual.
XX
PS   Claim 17; Page 13; 61pp; English.
XX
CC   The invention relates to G-protein coupled receptor 4 (GPR4) gene
CC   variants. The data about the GPR4 polynucleotides and polypeptides and
CC   the polymorphisms associated with them are useful for haplotyping at the
CC   GPR4 locus. Allele-specific oligonucleotide (ASO) is useful as probes and
CC   primers for assaying a polymorphism in GPR4 gene. The present sequence is
CC   a primer used to detect human GPR4 gene polymorphism
XX
SQ   Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGA 21
              | ||||||||
Db         10 TCTACAGGGA 1


RESULT 382
ABV84518/c
ID   ABV84518 standard; cDNA; 10 BP.
XX
AC   ABV84518;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Human HCC underexpressed gene SAGE tag #328.
XX
KW   SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW   CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW   expression pattern; differential expression; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002209591-A.
XX
PD   30-JUL-2002.
XX
PF   19-JAN-2001; 2001JP-00012328.
XX
PR   19-JAN-2001; 2001JP-00012328.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-631294/68.
XX
PT   Human chronic hepatitis C tissue expression exasperating gene group
PT   comprises 100 high-ranking genes.
XX
PS   Claim 28; Page 19; 139pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are differentially expressed in human
CC   chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC   hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC   The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC   located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC   polyA region of cDNAs derived from a variety of genes. These tags serve
CC   to uniquely identify each transcript and can thus be used to analyse the
CC   pattern of gene expression in particular cell types. The invention also
CC   relates to proteins encoded by the genes expressed in chronic hepatitis C
CC   liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC   the expression of groups of genes that are overexpressed in chronic
CC   hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC   in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC   treatment of these diseases. Such genes, inhibitors of their expression
CC   or activity, and antibodies against the gene products may be used in the
CC   development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC   ABV84491-ABV84590 are SAGE tags representing the 100 least highly
CC   expressed genes out of those genes which are underexpressed in
CC   hepatocellular carcinoma compared with normal liver tissue
XX
SQ   Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTCCA 26
              |||| |||||
Db         10 AGGGCGTCCA 1
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RESULT 383
ABV84755/c
ID   ABV84755 standard; cDNA; 10 BP.
XX
AC   ABV84755;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Chronic hepatitis C/HCC differentially expressed gene SAGE tag #565.
XX
KW   SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW   CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW   expression pattern; differential expression; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002209591-A.
XX
PD   30-JUL-2002.
XX
PF   19-JAN-2001; 2001JP-00012328.
XX
PR   19-JAN-2001; 2001JP-00012328.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-631294/68.
XX
PT   Human chronic hepatitis C tissue expression exasperating gene group
PT   comprises 100 high-ranking genes.
XX
PS   Claim 46; Page 26; 139pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are differentially expressed in human
CC   chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC   hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC   The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC   located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC   polyA region of cDNAs derived from a variety of genes. These tags serve
CC   to uniquely identify each transcript and can thus be used to analyse the
CC   pattern of gene expression in particular cell types. The invention also
CC   relates to proteins encoded by the genes expressed in chronic hepatitis C
CC   liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC   the expression of groups of genes that are overexpressed in chronic
CC   hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC   in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC   treatment of these diseases. Such genes, inhibitors of their expression
CC   or activity, and antibodies against the gene products may be used in the
CC   development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC   ABV84691-ABV84790 are SAGE tags representing the 100 least highly
CC   expressed genes out of those genes which are underexpressed in
CC   hepatocellular carcinoma compared with chronic hepatitis C liver tissue
XX
SQ   Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTCCA 26
                ||||  |||||
Db         10 AGGGCGTCCA 1


RESULT 384
ABV84794/c
ID   ABV84794 standard; cDNA; 10 BP.
XX
AC   ABV84794;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Human apolipoprotein G-III SAGE tag #604.
XX
KW   SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW   CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW   expression pattern; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002209591-A.
XX
PD   30-JUL-2002.
XX
PF   19-JAN-2001; 2001JP-00012328.
XX
PR   19-JAN-2001; 2001JP-00012328.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-631294/68.
XX
PT   Human chronic hepatitis C tissue expression exasperating gene group
PT   comprises 100 high-ranking genes.
XX
PS   Claim 55; Page 28; 139pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are differentially expressed in human
CC   chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC   hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC   The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC   located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC   polyA region of cDNAs derived from a variety of genes. These tags serve
CC   to uniquely identify each transcript and can thus be used to analyse the
CC   pattern of gene expression in particular cell types. The invention also
CC   relates to proteins encoded by the genes expressed in chronic hepatitis C
CC   liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC   the expression of groups of genes that are overexpressed in chronic
CC   hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC   in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC   treatment of these diseases. Such genes, inhibitors of their expression
CC   or activity, and antibodies against the gene products may be used in the
CC   development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC   ABV84791-ABV84890 are SAGE tags representing 100 genes which are highly
CC   expressed in chronic hepatitis C liver tissue
XX
SQ   Sequence 10 BP; 0 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
                |||||  ||||
Db         10 GGGAGGCCAG 1


RESULT 385
ABV84893/c
ID   ABV84893 standard; cDNA; 10 BP.
XX
AC   ABV84893;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Human apolipoprotein C-III SAGE tag #703.
XX
KW   SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW   CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW   expression pattern; ss.
XX
OS   Homo sapiens.
```

```
XX
PN   JP2002209591-A.
XX
PD   30-JUL-2002.
XX
PF   19-JAN-2001; 2001JP-00012328.
XX
PR   19-JAN-2001; 2001JP-00012328.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-631294/68.
XX
PT   Human chronic hepatitis C tissue expression exasperating gene group
PT   comprises 100 high-ranking genes.
XX
PS   Claim 64; Page 30; 139pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are differentially expressed in human
CC   chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC   hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC   The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC   located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC   polyA region of cDNAs derived from a variety of genes. These tags serve
CC   to uniquely identify each transcript and can thus be used to analyse the
CC   pattern of gene expression in particular cell types. The invention also
CC   relates to proteins encoded by the genes expressed in chronic hepatitis C
CC   liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC   the expression of groups of genes that are overexpressed in chronic
CC   hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC   in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC   treatment of these diseases. Such genes, inhibitors of their expression
CC   or activity, and antibodies against the gene products may be used in the
CC   development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC   ABV84891-ABV84990 are SAGE tags representing 100 genes which are highly
CC   expressed in hepatocellular carcinoma
XX
SQ   Sequence 10 BP; 0 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              ||||| ||||
Db         10 GGGAGGCCAG 1


RESULT 386
ABK81313
ID   ABK81313 standard; DNA; 10 BP.
XX
AC   ABK81313;
XX
DT   13-AUG-2002  (first entry)
XX
DE   Human ADMR gene allele-specific oligonucleotide PCR primer #10.
XX
KW   Human; G protein-coupled receptor similar to the adrenomedullin receptor;
KW   ADMR; haplotyping; haplotype pair; congestive heart failure; primer; ss;
KW   arterial hypertension; pulmonary hypertension; renal failure; sepsis;
KW   chromosome 12; single nucleotide polymorphism; PCR.
XX
OS   Homo sapiens.
XX
PN   WO200226770-A2.
XX
PD   04-APR-2002.
XX
PF   01-OCT-2001; 2001WO-US030879.
XX
PR   29-SEP-2000; 2000US-0236570P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Choi JY,  Lee HH,  Shah N;
XX
DR   WPI; 2002-435192/46.
XX
PT   Novel G-protein coupled receptor similar to the adrenomedullin receptor
PT   gene, useful therapeutically and in screening for drugs targeting
PT   receptor polypeptide.
XX
PS   Claim 16; Page 14; 78pp; English.
XX
CC   The invention relates to single nucleotide polymorphisms in the gene
CC   encoding the human G protein-coupled receptor similar to the
CC   adrenomedullin receptor (ADMR) polypeptide. A method for haplotyping the
CC   ADMR gene in an individual comprises identifying the nucleotide at one or
CC   more polymorphic sites and determining whether one of the copies of the
CC   gene is defined by one of the ADMR haplotypes given in the specification
CC   or whether both copies are defined by a haplotype pair. This method is
CC   useful in genotyping, whereby all possible haplotype pairs can be
CC   assigned to specific genotypes. An association between a trait and a
CC   haplotype or haplotype pair of the ADMR gene can be identified by
CC   comparing the frequency of the haplotype or haplotype pair in a
CC   population exhibiting the trait with the frequency of the haplotype or
CC   haplotype pair in a reference population, where a higher haplotype
CC   frequency in the trait population indicates the trait is associated with
CC   the haplotype or haplotype pair. ADMR and its corresponding DNA are used
CC   for studying the expression and function of ADMR, for use in screening
CC   for candidate drugs to treat diseases related to ADMR activity, such as
CC   congestive heart failure, arterial hypertension, pulmonary hypertension,
CC   renal failure, and sepsis. Sequences ABK81304-ABK81325 represent allele-
CC   specific oligonucleotide PCR primers used to detect ADMR gene
CC   polymorphisms
XX
SQ   Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAGTC 24
              | ||||||||
Db          1 AGAGGGAGTC 10


RESULT 387
AAD43418
ID   AAD43418 standard; DNA; 10 BP.
XX
AC   AAD43418;
XX
DT   14-NOV-2002  (first entry)
XX
DE   Human CYP3A5 gene polymorphism detecting primer #4.
XX
KW   Human; cytochrome P450; subfamily IIIA; polypeptide 5 isogene; CYP3A5;
KW   drug screening; polymorphism; haplotype; drug metabolising disorder;
KW   gene therapy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200246209-A2.
XX
PD   13-JUN-2002.
XX
PF   07-DEC-2001; 2001WO-US047218.
XX
PR   08-DEC-2000; 2000US-0254367P.
PR   03-MAY-2001; 2001US-0288470P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
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PI   Anastasio AE,  Han J,  Kliem SE,  Rounds E;
XX
DR   WPI; 2002-636448/68.
XX
PT   Novel isolated polynucleotide which is a polymorphic variant of
PT   cytochrome P450, subfamily IIIA, polypeptide 5 (CYP3A5) gene useful for
PT   expressing CYP3A5 protein isoform used in drug screening techniques.
XX
PS   Claim 17; Page 16; 127pp; English.
XX
CC   The invention relates to isolated polynucleotide having cytochrome P450,
CC   subfamily IIIA, polypeptide 5 isogene (CYP3A5). The invention is useful
CC   for screening drugs. The invention is useful for studying expression and
CC   function of CYP3A5 and expressing CYP3A5 protein for use in screening for
CC   candidate drugs to treat diseases related to CYP3A5 activity. The
CC   polymorphism and haplotype data is useful for validating whether CYP3A5
CC   is a suitable target for drugs to treat drug metabolising disorders,
CC   screening for such drugs and reducing bias in clinical trials of such
CC   drugs. The invention is also useful for therapeutic purposes. The
CC   invention is useful in studying the effect of variation on the biological
CC   activity of CYP3A5 as well as on the binding affinity of candidate drugs
CC   to CYP3A5, or for studying the enzymatic properties of such CYP3A5
CC   variants using these candidate drugs as substrate. The invention is
CC   useful in gene therapy. The present sequence is human CYP3A5 gene
CC   polymorphism detecting primer
XX
SQ   Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCAGG 28
              ||||||| |
Db          1 GGAGTCCAAG 10
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RESULT 388
ABK64079
ID   ABK64079 standard; DNA; 10 BP.
XX
AC   ABK64079;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human BF gene allele-specific oligonucleotide PCR primer #30.
XX
KW   Human; B-factor; properdin; BF; primer; ss; gene therapy; drug screening;
KW   antidiabetic; dermatological; diabetes; immunosuppressive;
KW   antiinflammatory; systemic lupus erythematosus.
XX
OS   Homo sapiens.
XX
PN   WO200218414-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US027098.
XX
PR   29-AUG-2000; 2000US-0228940P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Anastasio AE,  Finkel K,  Kazemi A,  Koshy B;
XX
DR   WPI; 2002-304244/34.
XX
PT   New genetic variants having polymorphisms in the B-Factor, Properdin (BF)
PT   gene, useful for studying the function of BF, and for treating disorders
PT   affected by expression or function of the BF isogene.
XX
PS   Claim 19; Page 16; 151pp; English.
XX
CC   The invention relates to single nucleotide polymorphisms in the gene
CC   encoding the human B-factor properdin protein (BF). A method for
CC   haplotyping the BF gene in an individual comprises identifying the
CC   nucleotide at one or more polymorphic sites and determining whether one
CC   of the copies of the gene is defined by one of the BF haplotypes given in
CC   the specification or whether both copies are defined by a haplotype pair.
CC   This method is useful in genotyping, whereby all possible haplotype pairs
CC   can be assigned to specific genotypes. An association between a trait and
CC   a haplotype or haplotype pair of the BF gene can be identified by
CC   comparing the frequency of the haplotype or haplotype pair in a
CC   population exhibiting the trait with the frequency of the haplotype or
CC   haplotype pair in a reference population, where a higher haplotype
CC   frequency in the trait population indicates the trait is associated with
CC   the haplotype or haplotype pair. BF and its corresponding DNA are used
CC   for studying the expression and function of BF, for use in screening for
CC   candidate drugs to treat diseases related to BF activity, such as
CC   diabetes and systemic lupus erythematosus. Sequences ABK64050-ABK64105
CC   represent allele-specific PCR primers used to detect human BF gene
CC   polymorphisms
XX
SQ   Sequence 10 BP; 3 A; 2 C; 5 G; 0 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAGTC 24
              |||||||| |
Db          1 ACAGGGAGGC 10
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RESULT 389
AAD25027
ID   AAD25027 standard; DNA; 10 BP.
XX
AC   AAD25027;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Human AANAT gene polymorphism detecting primer #17.
XX
KW   Human; genetic variant; arylalkylamine N-acetyltransferase; AANAT gene;
KW   haplotyping; genotyping; pineal gland disorder; melatonin synthesis;
KW   gene therapy; antisense therapy; primer; polymorphism; ss.
XX
OS   Homo sapiens.
XX
PN   WO200187909-A2.
XX
PD   22-NOV-2001.
XX
PF   18-MAY-2001; 2001WO-US016279.
XX
PR   18-MAY-2000; 2000US-0205068P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Choi JY,  Kazemi A,  Nandabalan K;
XX
DR   WPI; 2002-055682/07.
XX
PT   New genetic variants of human arylalkylamine N-acetyltransferase (AANAT)
PT   gene for studying expression, function of the gene and expressing AANAT
PT   protein for use in screening for drugs to treat disorders of pineal
PT   gland.
XX
PS   Claim 18; Page 13; 67pp; English.
XX
CC   The patent discloses novel genetic variants of the arylalkylamine N-
CC   acetyltransferase (AANAT) gene. The invention also relates to
CC   compositions and methods for haplotyping and/or genotyping the AANAT
CC   gene. Polymorphic variants of AANAT protein are useful for screening for
CC   drugs targeting the polypeptide. AANAT polynucleotides are useful for
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CC   studying the expression and function of AANAT and for expressing AANAT
CC   protein for use in screening for candidate drugs to treat diseases
CC   related to AANAT activity. The methods are used to develop diagnostic
CC   tests and therapeutic treatment for disorders of pineal gland that derive
CC   from defects in melatonin synthesis. It is useful for determining whether
CC   an individual has one of the haplotypes 1-4 or the haplotype pairs. The
CC   haplotyping method is useful to validate AANAT as a candidate target for
CC   treating a specific condition or disease predicted to be associated with
CC   AANAT activity. AANAT sequences of the invention are also used in gene
CC   therapy and antisense therapy. The present DNA sequence is a primer which
CC   is used for detecting human AANAT gene polymorphisms
XX
SQ   Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCC 25
                ||||||| ||
Db          1 CAGGGAGGCC 10


RESULT 390
AAD32316
ID   AAD32316 standard; DNA; 10 BP.
XX
AC   AAD32316;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human neurotrophin 3 (NTF3) gene polymorphism detecting primer #2.
XX
KW   Human; genetic variant; neurotrophin 3; NTF3; haplotyping; genotyping;
KW   nervous system disorder; congenital heart defect; gene therapy;
KW   therapeutic; polymorphism; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200212499-A2.
XX
PD   14-FEB-2002.
XX
PF   06-AUG-2001; 2001WO-US024665.
XX
PR   04-AUG-2000; 2000US-0223208P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Kliem SE,  Koshy B,  Lanz EM;
XX
DR   WPI; 2002-269092/31.
XX
PT   Novel polymorphic variants of neurotrophin 3 (NTF3), useful for studying
PT   the expression and function of NTF3, and for screening candidate drugs to
PT   treat nervous system disorders and congenital heart defects.
XX
PS   Claim 19; Page 13; 60pp; English.
XX
CC   The present invention relates to genetic variants of human neurotrophin
CC   (NTF) 3 gene. The invention also relates to compositions and methods for
CC   haplotyping and/or genotyping the NTF3 gene in an individual. Sequences
CC   of the invention are useful for studying the expression and function of
CC   NTF3 protein for use in screening for candidate drugs to treat diseases
CC   related to NTF3 activity. The polymorphism and haplotype data is useful
CC   for validating whether NTF3 is a suitable target for drugs to treat
CC   nervous system disorders and congenital heart defects, screening for such
CC   drugs and reducing bias in clinical trials of such drugs. They are also
CC   useful for therapeutic purposes. The haplotyping method is useful for
CC   improving the efficiency and outcome of several steps in the discovery
CC   and development of drugs for treating diseases associated with NTF3
CC   activity such as nervous system disorders and congenital heart defects.
CC   It is also useful for validating NTF3 as a candidate target for treating
CC   a specific condition or disease predicted to be associated with NTF3
CC   activity. The method is also useful for screening compounds to treat a
CC   specific condition or disease predicted to be associated with NTF3
CC   activity. Sequences of the invention are also used in gene therapy. The
CC   present DNA sequence is a primer used to detect human NTF3 gene
CC   polymorphisms
XX
SQ   Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCTAC 10
                ||||||| |
Db          1 CGGGCCCTCC 10


RESULT 391
AAD47781/c
ID   AAD47781 standard; DNA; 10 BP.
XX
AC   AAD47781;
XX
DT   24-FEB-2003  (first entry)
XX
DE   Human GNB3 gene polymorphisms detecting primer #1.
XX
KW   Human; guanine nucleotide binding protein beta polypeptide 3; G protein;
KW   GNB3; polymorphism; obesity; left ventricular hypertrophy; hypertension;
KW   drug discovery; cardiovascular; development process; asthma; anorectic;
KW   gene therapy; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200277284-A1.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2001; 2001WO-US008961.
XX
PR   21-MAR-2001; 2001WO-US008961.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bentivegna SC,  Choi JY,  Kliem SE,  Koshy B;
XX
DR   WPI; 2003-018947/01.
XX
PT   New genetic variants having polymorphisms in the G protein, GNB3 gene,
PT   useful for treating disorders with abnormal expression or function of the
PT   GNB3 gene, such as asthma, obesity, hypertension and left ventricular
PT   hypertrophy.
XX
PS   Claim 18; Page 15; 88pp; English.
XX
CC   The invention relates to an isolated polypeptide which comprises a first
CC   nucleotide sequence which is a polymorphic variant of a reference
CC   sequence for the guanine nucleotide binding protein (G protein), beta
CC   polypeptide 3 (GNB3) gene or fragment. Polymorphic variants of the GNB3
CC   gene are useful in studying the expression and biological function of
CC   GNB3 and in identifying drugs targetting GNB3 protein for treating
CC   disorders associated with abnormal expression or function of GNB3, e.g.
CC   hypertension, obesity, asthma and left ventricular hypertrophy.
CC   Polynucleotides comprising a polymorphic gene variant or fragment may be
CC   used for therapeutic purposes, where a patient could benefit from
CC   expression or increased expression of a particular GNB3 gene isoform or
CC   an expression vector encoding the isoform may be administered to the
CC   patient. Haplotype information is useful in improving the efficiency and
CC   output of several steps in drug discovery and development process,
CC   including target validation, identifying lead compounds and early phase
CC   clinical trials. The invention is used in gene therapy. The present
CC   sequence is human GNB3 gene polymorphisms detecting primer
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```
XX
SQ   Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAG 22
              || |||||||
Db         10 GTTCAGGGAG 1


RESULT 392
ACC78765
ID   ACC78765 standard; DNA; 10 BP.
XX
AC   ACC78765;
XX
DT   02-SEP-2003  (first entry)
XX
DE   Normal estrogen responsive cells derived SAGE tag.
XX
KW   ERE; reporter construct; estrogen response element; cytostatic; rat;
KW   gene therapy; breast cancer; SAGE; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003042364-A2.
XX
PD   22-MAY-2003.
XX
PF   08-NOV-2002; 2002WO-US035901.
XX
PR   09-NOV-2001; 2001US-0338136P.
XX
PA   (DAND ) DANA FARBER CANCER INST INC.
XX
PI   Polyak K,  Pankaj S;
XX
DR   WPI; 2003-449570/42.
XX
PT   New reporter construct for identifying and isolating estrogen-responsive
PT   cells comprises an estrogen response segment, a promoter segment and a
PT   nucleotide sequence that encodes a reporter polypeptide.
XX
PS   Example 4; Page 32; 51pp; English.
XX
CC   The invention relates to a reporter construct comprising: (a) an estrogen
CC   response segment having 5 or more estrogen response elements (ERE); (b) a
CC   promoter segment having at least one promoter nucleic acid sequence; and
CC   (c) a nucleotide sequence that encodes a reporter polypeptide, where the
CC   nucleotide sequence is operably linked to the promoter segment and the
CC   estrogen response segment. The reporter construct and vector are useful
CC   in identifying and isolating estrogen-responsive cells. The methods are
CC   useful in inhibiting the proliferation or survival of estrogen-responsive
CC   breast cancer cells or in enhancing the proliferation or survival of
CC   estrogen-receptor non-expressing, estrogen-non-responsive cells.
CC   Sequences ACC78740-75 represent SAGE tags for transcripts specifically or
CC   most abundantly expressed in normal estrogen responsive cells
XX
SQ   Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCTAC 10
              | ||||||||
Db          1 CCGGCCCTAC 10


RESULT 393
AAD53538
ID   AAD53538 standard; DNA; 10 BP.
XX
AC   AAD53538;
XX
DT   28-MAY-2003  (first entry)
XX
DE   Human GNRH2 gene polymorphism detecting primer #14.
XX
KW   Human; gonadotropin-releasing hormone 2; GNRH2; reproductive disorder;
KW   gynaecological; cytostatic; hormonal; target validation; gene therapy;
KW   drug screening; lead compound; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200294850-A2.
XX
PD   28-NOV-2002.
XX
PF   01-NOV-2001; 2001WO-US050630.
XX
PR   18-MAY-2001; 2001WO-US016353.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Duda A,  Kliem SE,  Nandabalan K,  Sausker EA;
XX
DR   WPI; 2003-148454/14.
XX
PT   New gonadotropin-releasing hormone 2 (GNRH2) polypeptide encoded by
PT   genetic variants having polymorphisms in the GNRH2 gene, for studying the
PT   function of, and treating disorders, such as, reproductive disorders.
XX
PS   Claim 16; Col 14; 33pp; English.
XX
CC   The invention relates to gonadotropin-releasing hormone 2 (GNRH2) and its
CC   nucleic acid sequence. Polymorphic variants of the GNRH2 gene are useful
CC   in studying the expression and function of GNRH2, and in expressing GNRH2
CC   proteins for use in screening candidate drugs for treating diseases
CC   associated with GNRH2 activity, such as reproductive disorders.
CC   Polynucleotides comprising a polymorphic gene variant or fragment may be
CC   used for therapeutic purposes, where a patient could benefit from
CC   expression or increased expression of a particular GNRH2 protein isoform,
CC   or an expression vector encoding the isoform may be administered to the
CC   patient. Haplotype information is useful in improving the efficiency and
CC   output of several steps in a drug discovery and development process,
CC   including target validation, identifying lead compounds, and early phase
CC   clinical trials. GNRH2 gene is used in gene therapy. The present sequence
CC   is a primer used for detecting human GNRH2 gene polymorphisms
XX
SQ   Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGG 20
              |||| |||||
Db          1 GTGTCCAGGG 10


RESULT 394
AAD60113
ID   AAD60113 standard; DNA; 10 BP.
XX
AC   AAD60113;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human androgen-regulated gene (ARG) transcription regulator #2.
XX
KW   Human; androgen-regulated gene; ARG; PMEPA1; prostate cancer; ss.
XX
OS   Homo sapiens.
```

```
XX
PN   US6566130-B1.
XX
PD   20-MAY-2003.
XX
PF   26-JAN-2001; 2001US-00769482.
XX
PR   28-JAN-2000; 2000US-0178772P.
PR   31-JAN-2000; 2000US-0179045P.
XX
PA   (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
PI   Srivastava S,  Moul JW,  Xu LL,  Segawa T;
XX
DR   WPI; 2003-719644/68.
XX
PT   Novel isolated androgen-regulated gene designated as PMEPA1 useful for
PT   selecting primers and probes for detecting prostate cancer cells in
PT   biological samples by nucleic acid amplification techniques.
XX
PS   Example 7; Col 69; 58pp; English.
XX
CC   The invention relates to an isolated androgen-regulated gene (ARG)
CC   designated as PMEPA1. The invention is useful for selecting primers and
CC   probes for detecting prostate cancer cells in a biological sample by
CC   using nucleic acid amplification techniques. The present sequence is
CC   human ARG transcription regulator oligonucleotide
XX
SQ   Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAG 22
              || |||||||
Db          1 GTGCAGGGAG 10


RESULT 395
ADD71263/c
ID   ADD71263 standard; DNA; 10 BP.
XX
AC   ADD71263;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Mouse ET gene 5' splice donor site from intron 4.
XX
KW   Mouse; ethenolaminephosphate cytidilyl transferase; ET; ds;
KW   splice donor site; antilipemic; cardiant; anorectic;
KW   phosphatidylethanolamine; Zellweger's syndrome; lipid-related disease;
KW   cardiovascular disease; atherosclerosis; obesity.
XX
OS   Mus musculus.
XX
PN   US2003194795-A1.
XX
PD   16-OCT-2003.
XX
PF   21-MAR-2002; 2002US-00101957.
XX
PR   21-MAR-2002; 2002US-00101957.
XX
PA   (BAKO/) BAKOVIC M.
PA   (POLO/) POLOUMIENKO A.
XX
PI   Bakovic M,  Poloumienko A;
XX
DR   WPI; 2003-844457/78.
XX
PT   New gene encoding a protein having ethanolaminephosphate
PT   cytidyltransferase activity, useful for treating Zellweger's syndrome, or
PT   lipid-related diseases such as cardiovascular diseases and obesity.
XX
PS   Example 1; Page 6; 22pp; English.
XX
CC   The invention relates to a mouse gene encoding a protein having
CC   ethanolaminephosphate cytidyltransferase (ET) activity appearing as
CC   ADD71226, a degenerate variant of the ET gene, or a sequence that
CC   hybridises to the complement of the ET gene under stringent conditions.
CC   Also included is a promoter of a human ethanolaminephosphate
CC   cytidyltransferase gene appearing as ADD71227. The gene and promoter are
CC   useful for producing a transgenic animal, and for identifying,
CC   preventing, and treating diseases (by gene therapy) related to
CC   inappropriate phosphatidylethanolamine production, e.g. Zellweger's
CC   syndrome, or lipid-related diseases such as cardiovascular diseases,
CC   atherosclerosis and obesity. The present sequence is a mouse ET gene 5'
CC   splice donor site.
XX
SQ   Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTA 15
              ||||| ||||
Db         10 CCTACCTGTA 1


RESULT 396
ADE27823/c
ID   ADE27823 standard; DNA; 10 BP.
XX
AC   ADE27823;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human B7-2 mRNA targeted oligonucleotide SEQ ID 85.
XX
KW   ss; human; B7-2; inflammatory skin disorder; antisense; psoriasis;
KW   contact dermatitis; atopic dermatitis; seborrheic dermatitis;
KW   nummular dermatitis; generalised exfoliative dermatitis; eczema;
KW   critical costimulatory molecule.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US2003176374-A1.
XX
PD   18-SEP-2003.
XX
PF   09-MAY-2001; 2001US-00851871.
XX
PR   31-DEC-1996;   96US-00777266.
PR   04-JUN-1999;   99US-00326186.
PR   25-MAY-2000; 2000WO-US014471.
XX
PA   (BENN/) BENNETT C F.
PA   (VICK/) VICKERS T A.
PA   (KARR/) KARRAS J G.
XX
PI   Bennett CF,  Vickers TA,  Karras JG;
XX
DR   WPI; 2003-863863/80.
XX
PT   Treating an inflammatory skin disorder such as psoriasis comprises
PT   topically applying an antisense compound targeted to the nucleic acid
PT   encoding human B7 protein.
XX
PS   Example 1; SEQ ID NO 85; 88pp; English.
XX
CC   The invention relates to a method of treating an inflammatory skin
CC   disorder in an individual by topically applying an antisense compound
CC   targeted to a nucleic acid molecule encoding a human B7 protein. The
```

```
CC   invention is for treating an inflammatory skin disorder in individual.
CC   The skin disorder is psoriasis, contact dermatitis, atopic dermatitis,
CC   seborrheic dermatitis, nummular dermatitis, generalised exfoliative
CC   dermatitis or eczema. The invention effectively modulates critical
CC   costimulatory molecules such as the B7 protein. The present sequence
CC   represents a human B7-2 targeted oligonucleotide.
XX
SQ   Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          13 GTACAGGGAG 22
               |||| |||||
Db          10 GTACGGGGAG 1


RESULT 397
AAV48047/c
ID   AAV48047 standard; DNA; 11 BP.
XX
AC   AAV48047;
XX
DT   19-OCT-1998  (first entry)
XX
DE   Human B7-2 targetted oligonucleotide 10992.
XX
KW   ss; human; B7; T cell; inflammation; autoimmune disease; cell activation;
KW   cell proliferation.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .11
FT                    /*tag=  a
FT                    /note= "Phosphorothioate linkages"
XX
PN   WO9829124-A1.
XX
PD   09-JUL-1998.
XX
PF   16-DEC-1997;   97WO-US023270.
XX
PR   31-DEC-1996;   96US-00777266.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Vickers TA;
XX
DR   WPI; 1998-387783/33.
XX
PT   New oligo:nucleotide(s) that modulate expression of B7 proteins - used
PT   for, e.g. controlling activation and proliferation of T cells,
PT   particularly for treatment, diagnosis and prevention of inflammation.
XX
PS   Example 1; Page 39; 120pp; English.
XX
CC   The oligonucleotides which specifically hybridise to B7 modulate its
CC   expression (and thus T cell activation and proliferation). This is
CC   particularly useful for treatment and prevention of inflammation and
CC   autoimmune diseases, e.g. asthma, (juvenile) diabetes, myasthenia gravis,
CC   Grave's disease, rheumatoid arthritis, allograft rejection, psoriasis,
CC   (systemic) lupus erythematosus, multiple sclerosis, contact dermatitis,
CC   rhinitis, allergy, cancer and metastases. The oligonucleotides may also
CC   be used to manipulate T cell activation ex vivo; to determine or detect
CC   B7 protein expression; for diagnosis; as assay and purification reagents,
CC   and to study physiological roles of B7 proteins
XX
SQ   Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          13 GTACAGGGAG 22
               |||| |||||
Db          11 GTACGGGGAG 2


RESULT 398
AAZ18735/c
ID   AAZ18735 standard; DNA; 11 BP.
XX
AC   AAZ18735;
XX
DT   22-OCT-1999  (first entry)
XX
DE   Murine C57BL/6 SAGE tag 3496724.
XX
KW   Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
KW   healing response; microsatellite marker; treatment; central nerve;
KW   peripheral nerve; nerve injury; SAGE tag; murine; ss.
XX
OS   Mus sp.
XX
PN   WO9941364-A2.
XX
PD   19-AUG-1999.
XX
PF   12-FEB-1999;   99WO-US002962.
XX
PR   13-FEB-1998;   98US-0074737P.
PR   26-AUG-1998;   98US-0097937P.
PR   28-SEP-1998;   98US-0102051P.
XX
PA   (WIST-) WISTAR INST.
XX
PI   Heber-Katz E;
XX
DR   WPI; 1999-494533/41.
XX
PT   New mammalian model for enhanced wound healing - useful for identifying
PT   enhanced wound healing genes.
XX
PS   Claim 13; Page 56; 136pp; English.
XX
CC   This invention describes a novel non-MRL healer mouse (M) having at least
CC   one quantitative trait locus selected from those given in the
CC   specification, exhibiting an enhanced healing response to a wound
CC   compared to mice (m) without the locus. The invention describes a novel
CC   method of identifying a gene involved in enhanced wound healing by
CC   identifying DNA microsatellite markers which can distinguish healer mice
CC   from non-healer mice and identifying microsatellite markers which
CC   segregate with enhanced wound healing in progeny of the mice, where a
CC   chromosomal locus containing at least one enhanced wound healing gene is
CC   identified. A method of treating a wound in a mammal is also disclosed.
CC   The new methods are useful for treating wounds, especially central and
CC   peripheral nerve wound. The methods of the invention are useful for
CC   restoring function after nerve injury in a mammal. (M) is useful as a
CC   mammalian model of enhanced wound healing, useful for identifying genes
CC   and gene products involved in enhanced wound healing, and to provide
CC   methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags
CC   from C57BL/6 and MRL mice which are used to illustrate the method of the
CC   invention
XX
SQ   Sequence 11 BP; 2 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGA 21
               ||||| ||||
Db          10 TGTACGGGGA 1
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RESULT 399
AAA35948
ID   AAA35948 standard; DNA; 11 BP.
XX
AC   AAA35948;
XX
DT   26-JUL-2000  (first entry)
XX
DE   Human genomic DNA single copy SNP oligonucleotide SEQ ID NO:5.
XX
KW   Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
KW   allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
KW   genomic classification; identification; DNA fingerprinting;
KW   tumour characterisation; hybridisation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200018960-A2.
XX
PD   06-APR-2000.
XX
PF   24-SEP-1999;  99WO-US022283.
XX
PR   25-SEP-1998;  98US-0101757P.
XX
PA   (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
PI   Landers JE,  Jordan B,  Housman DE,  Charest A;
XX
DR   WPI; 2000-293181/25.
XX
PT   Detection of single nucleotide polymorphisms in genomes by preparation
PT   and analysis of reduced complexity genomes, useful for genotyping,
PT   fingerprinting and determining allele frequency of SNPs.
XX
PS   Example 1; Page 77; 111pp; English.
XX
CC   A method has been developed for detecting the presence or absence of a
CC   single nucleotide polymorphism (SNP) allele in a genomic sample. The
CC   method comprises preparing a reduced complexity genome (RCG) from the
CC   genomic sample and analysing the RCG for the presence or absence of a SNP
CC   allele. The method can be used to characterise a tumour, to generate a
CC   genomic pattern for an individual genome or to generate a genomic
CC   classification code for a genome. The method can be used to assess
CC   whether a subject is at risk for developing a disease or to identify a
CC   set of SNP alleles associated with a disease. The method can also be used
CC   to perform linkage analysis. AAA35944 to AAA35947 represent sequences
CC   used in the exemplification of the present invention. AAA35948 to
CC   AAA36632 represent nucleotide sequences containing SNPs
XX
SQ   Sequence 11 BP; 5 A; 1 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match          30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACA 17
              || |||||||
Db          1 TAAGTGTACA 10


RESULT 400
AAC63231
ID   AAC63231 standard; DNA; 11 BP.
XX
AC   AAC63231;
XX
DT   06-FEB-2001  (first entry)
XX
DE   Oligonucleotide #4 used in a method for primer selection.
XX
KW   PCR primer; nucleic acid amplification; melting temperature; T_m; ss.
XX
OS   Homo sapiens.
XX
PN   WO200060123-A2.
XX
PD   12-OCT-2000.
XX
PF   05-APR-2000; 2000WO-US008962.
XX
PR   06-APR-1999;   99US-0127891P.
XX
PA   (GENO-) GENOME TECHNOLOGIES LLC.
XX
PI   Senapathy P;
XX
DR   WPI; 2000-656235/63.
XX
PT   Determining Tm range for several degenerate primers with a fixed-sequence
PT   and a degenerate-sequence portion for use in polymerase chain reaction
PT   amplification by identifying a specific sequence in the nucleic acid
PT   template.
XX
PS   Disclosure; Fig 2; 34pp; English.
XX
CC   The present invention relates to a method for selecting PCR primers for
CC   nucleic acid amplification. The method comprises determining the melting
CC   temperature (T_m) range for degenerate oligonucleotide primers with a
CC   fixed-sequence portion (FS) and a degenerate-sequence portion (DS) by
CC   searching known portion of a nucleic acid template for a sequence
CC   complementary to a desired FS of a primer. Nucleotide base pairs flanking
CC   or interspersed between the sequence complementary to a DS of one of the
CC   primers are detected and T_m is calculated. The method of the present
CC   invention allows primers which produce more efficient DNA amplification
CC   to be produced. The present sequence is a primer. This sequence was used
CC   to exemplify the occurence of a primer with a FS of 6 base pairs (CGGCCC)
CC   within a template. The remaining 5 base pairs make up the DS
XX
SQ   Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match          30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GGCCCTACGT 12
              ||||||||| |
Db          2 GGCCCTACCT 11


RESULT 401
AAF32889/c
ID   AAF32889 standard; DNA; 11 BP.
XX
AC   AAF32889;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Human B7-2 mRNA antisense oligonucleotide SEQ ID NO: 86.
XX
KW   Human; mouse; B7-1; B7-2; antisense; PCR primer; inflammation;
KW   autoimmune disorder; phosphorothioate backbone; ss.
XX
OS   Homo sapiens.
XX
PN   WO200074687-A1.
XX
PD   14-DEC-2000.
XX
PF   25-MAY-2000; 2000WO-US014471.
XX
PR   04-JUN-1999;   99US-00326186.
XX
PA   (ISIS-) ISIS PHARM INC.
```

```
XX
PI   Bennett CF,  Vickers TA,  Karras JG;
XX
DR   WPI; 2001-049991/06.
XX
PT   Novel compound for diagnosing, preventing and treating immune disorders,
PT   comprising an oligonucleotide that specifically hybridizes with a nucleic
PT   acid sequence encoding B7 protein.
XX
PS   Example 1; Page 51; 162pp; English.
XX
CC   The present invention provides sequences of antisense oligonucleotides
CC   targeted at the murine and human B7-1 and B7-2 coding and mRNA sequences.
CC   The antisense sequences have phosphorothioate backbones and some
CC   nucleotides are 2'-methoxyethoxy residues. The sequences can be used in
CC   the treatment of inflammatory and autoimmune disorders, including asthma,
CC   juvenile diabetes mellitus, myasthenia gravis, Graves' disease,
CC   rheumatoid arthritis, allograft rejection, inflammatory bowel disease,
CC   multiple sclerosis, psoriasis, systemic lupus erythematosus, contact
CC   dermatitis, rhinitis, allergies and cancer
XX
SQ   Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAG 22
              |||| |||||
Db         11 GTACGGGGAG 2


RESULT 402
AAF31235
ID   AAF31235 standard; DNA; 11 BP.
XX
AC   AAF31235;
XX
DT   09-APR-2001  (first entry)
XX
DE   Novel BAC vector construction restriction site #4.
XX
KW   BAC vector; copy number; cloning; gene expression; pTRANS; pTRANS-SacB;
KW   pBacTA.PUC2; ds.
XX
OS   Synthetic.
XX
PN   WO200078977-A1.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-US016767.
XX
PR   18-JUN-1999;   99US-0140287P.
XX
PA   (AVET ) AVENTIS PHARM INC.
XX
PI   Grossman T,  Macneil I,  August P;
XX
DR   WPI; 2001-102727/11.
XX
PT   Novel vector for increasing copy number and gene expression in plasmids,
PT   comprises transposable element containing high copy number origin of
PT   replication capable of in vitro transposition into target plasmid.
XX
PS   Disclosure; Fig 7; 40pp; English.
XX
CC   The present invention describes a vector for increasing the copy number
CC   of plasmids, comprising a transposable element containing a high copy
CC   number origin of replication capable of transposition into a target
CC   plasmid. The vector may be pTRANS-SacB, pTRANS or pBacTA.PUC2. The vector
CC   can be used to facilitate the cloning of large inserts into BAC plasmids,
CC   including full-length genes, the isolation of large amounts of BAC DNA
CC   and the increased expression of BAC genes. They can also be used to
CC   generate shuttle vectors without cloning
XX
SQ   Sequence 11 BP; 4 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         15 ACAGGGAGTC 24
              |||| |||||
Db          2 ACAGAGAGTC 11


RESULT 403
AAS02836
ID   AAS02836 standard; DNA; 11 BP.
XX
AC   AAS02836;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Human pregnane X receptor (hPXR) gene, PCR primer #106.
XX
KW   Human; pregnane X receptor; hPXR; PCR primer; diagnostic; cancer;
KW   therapeutic; chemotherapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200120026-A2.
XX
PD   22-MAR-2001.
XX
PF   08-SEP-2000; 2000WO-EP008827.
XX
PR   10-SEP-1999;   99EP-00118120.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI   Wojnowski L,  Hustert E;
XX
DR   WPI; 2001-273428/28.
XX
PT   Novel variant of the human pregnane X receptor gene, associated with
PT   insufficient metabolization and/or sensitivity to drugs, is useful for
PT   diagnosing and treating diseases with drugs that are modulators of their
PT   gene product.
XX
PS   Claim 37; Page 45; 108pp; English.
XX
CC   AAS02731-AAS02909 represent human pregnane X receptor (hPXR) coding
CC   sequences and PCR primers of the invention. The human pregnane X receptor
CC   sequences are used to make antibodies, or a substance capable of binding
CC   specifically to the gene product of hPXR gene, for diagnosing and
CC   treating various diseases, such as cancer, with drugs that are
CC   substrates, inhibitors or modulators of the hPXR gene product. The
CC   proteins can be used to identify and obtain prodrugs and drugs for
CC   treatment of diseases which are amenable to chemotherapy. The nucleic
CC   acids can be used in gene therapy for the treatment or prevention of
CC   disorders associated with hPXR expression
XX
SQ   Sequence 11 BP; 2 A; 1 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              |||||| |||
Db          2 GGGAGTGCAG 11


RESULT 404
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AAS02837/c
ID   AAS02837 standard; DNA; 11 BP.
XX
AC   AAS02837;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Human pregnane X receptor (hPXR) gene, PCR primer #107.
XX
KW   Human; pregnane X receptor; hPXR; PCR primer; diagnostic; cancer;
KW   therapeutic; chemotherapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200120026-A2.
XX
PD   22-MAR-2001.
XX
PF   08-SEP-2000; 2000WO-EP008827.
XX
PR   10-SEP-1999;   99EP-00118120.
XX
PA   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI   Wojnowski L,  Hustert E;
XX
DR   WPI; 2001-273428/28.
XX
PT   Novel variant of the human pregnane X receptor gene, associated with
PT   insufficient metabolization and/or sensitivity to drugs, is useful for
PT   diagnosing and treating diseases with drugs that are modulators of their
PT   gene product.
XX
PS   Claim 37; Page 45; 108pp; English.
XX
CC   AAS02731-AAS02909 represent human pregnane X receptor (hPXR) coding
CC   sequences and PCR primers of the invention. The human pregnane X receptor
CC   sequences are used to make antibodies, or a substance capable of binding
CC   specifically to the gene product of hPXR gene, for diagnosing and
CC   treating various diseases, such as cancer, with drugs that are
CC   substrates, inhibitors or modulators of the hPXR gene product. The
CC   proteins can be used to identify and obtain prodrugs and drugs for
CC   treatment of diseases which are amenable to chemotherapy. The nucleic
CC   acids can be used in gene therapy for the treatment or prevention of
CC   disorders associated with hPXR expression
XX
SQ   Sequence 11 BP; 2 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              |||||| |||
Db         10 GGGAGTGCAG 1


RESULT 405
ABQ86448/c
ID   ABQ86448 standard; cDNA; 11 BP.
XX
AC   ABQ86448;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 203.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 45; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAG 22
              || |||||||
Db         10 GTTCAGGGAG 1


RESULT 406
ABQ86579
ID   ABQ86579 standard; cDNA; 11 BP.
XX
AC   ABQ86579;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 334.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
```

```
PS   Claim 8; Page 50; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              |||| |||||
Db          2 GGGACTCCAG 11


RESULT 407
ABQ86675
ID   ABQ86675 standard; cDNA; 11 BP.
XX
AC   ABQ86675;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 430.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 54; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 2 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCAGG 28
              |||| |||||
Db          2 GGAGGCCAGG 11


RESULT 408
ABQ87015/c
ID   ABQ87015 standard; cDNA; 11 BP.
XX
AC   ABQ87015;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 770.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 69; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCC 25
              ||| ||||||
Db         11 CAGTGAGTCC 2


RESULT 409
ABQ86467
ID   ABQ86467 standard; cDNA; 11 BP.
XX
AC   ABQ86467;
XX
DT   10-SEP-2002  (first entry)
```

XX
DE Human skin stress/ageing related EST SEQ ID NO 222.
XX
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253773-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015178.
XX
PR 03-JAN-2001; 2001DE-01000121.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-528865/56.
XX
PT Identifying genes involved in skin stress and aging, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential gene
PT expression.
XX
PS Claim 8; Page 46; 325pp; German.
XX
CC The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ Sequence 11 BP; 1 A; 7 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGGGCCCTAC 10
|||||||||
Db 1 CCGGCCCTAC 10

RESULT 410
ABV68538/c
ID ABV68538 standard; cDNA; 11 BP.
XX
AC ABV68538;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 6324.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 201; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 15 ACAGGGAGTC 24
|||| |||||
Db 10 ACAGAGAGTC 1

RESULT 411
ABV63286/c
ID ABV63286 standard; cDNA; 11 BP.
XX
AC ABV63286;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 1072.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 54; 1345pp; German.
XX

```
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          13 GTACAGGGAG 22
               || |||||||
Db          10 GTTCAGGGAG 1


RESULT 412
ABV71898/c
ID   ABV71898 standard; cDNA; 11 BP.
XX
AC   ABV71898;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 9684.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 313; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           9 ACGTGTACAG 18
                 | ||||||||
Db          11 AGGTGTACAG 2


RESULT 413
ABV64207
ID   ABV64207 standard; cDNA; 11 BP.
XX
AC   ABV64207;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 1993.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 80; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 7 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           1 CGGGCCCTAC 10
                 |||||||||
Db           1 CCGGCCCTAC 10


RESULT 414
ABV70008
```

```
ID   ABV70008 standard; cDNA; 11 BP.
XX
AC   ABV70008;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7794.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 248; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTG 13
              ||||||| ||
Db          1 GCCCTACCTG 10


RESULT 415
ABV70593
ID   ABV70593 standard; cDNA; 11 BP.
XX
AC   ABV70593;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 8379.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 268; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCAGG 28
              ||| ||||||
Db          2 GGAATCCAGG 11


RESULT 416
ABV62919/c
ID   ABV62919 standard; cDNA; 11 BP.
XX
AC   ABV62919;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 705.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
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```
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 44; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match          30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          11 GTGTACAGGG 20
               | ||||||||
Db          11 GAGTACAGGG 2


RESULT 417
ABV71628
ID   ABV71628 standard; cDNA; 11 BP.
XX
AC   ABV71628;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 9414.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 303; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 7 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match          30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCTAC 10
              | ||||||||
Db          1 CCGGCCCTAC 10


RESULT 418
ABV64991
ID   ABV64991 standard; cDNA; 11 BP.
XX
AC   ABV64991;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 2777.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  .
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 102; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match          30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          18 GGGAGTCCAG 27
               |||| |||||
Db           2 GGGACTCCAG 11


RESULT 419
ABV69231/c
ID   ABV69231 standard; cDNA; 11 BP.
XX
AC   ABV69231;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7017.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 220; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          16 CAGGGAGTCC 25
               ||| ||||||
Db          11 CAGTGAGTCC 2


RESULT 420
ABV63172
ID   ABV63172 standard; cDNA; 11 BP.
XX
AC   ABV63172;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 958.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 51; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          19 GGAGTCCAGG 28
               ||| ||||||
Db           2 GGAATCCAGG 11


RESULT 421
ABV62587
ID   ABV62587 standard; cDNA; 11 BP.
XX
AC   ABV62587;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 373.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
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PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 36; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GCCCTACGTG 13
              ||||||| ||
Db          1 GCCCTACCTG 10


RESULT 422
ABV62625/c
ID   ABV62625 standard; cDNA; 11 BP.
XX
AC   ABV62625;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 411.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 37; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         18 GGGAGTCCAG 27
              ||||||| ||
Db         11 GGGAGTCAAG 2


RESULT 423
ABV64477/c
ID   ABV64477 standard; cDNA; 11 BP.
XX
AC   ABV64477;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 2263.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 88; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
```

```
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 ACGTGTACAG 18
              | ||||||||
Db         11 AGGTGTACAG 2


RESULT 424
ABV66356
ID   ABV66356 standard; cDNA; 11 BP.
XX
AC   ABV66356;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4142.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 140; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGG 20
              |||| |||||
Db          2 GTGTTCAGGG 11


RESULT 425
ABV68439
ID   ABV68439 standard; cDNA; 11 BP.
XX
AC   ABV68439;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 6225.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 198; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCAGG 28
              |||| |||||
Db          2 GGAGGCCAGG 11


RESULT 426
ABV70340/c
ID   ABV70340 standard; cDNA; 11 BP.
XX
AC   ABV70340;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 8126.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
```

KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 259; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

```
  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          11 GTGTACAGGG 20
               | ||||||||
Db          11 GAGTACAGGG 2
```

RESULT 427
ABV70707/c
ID ABV70707 standard; cDNA; 11 BP.
XX
AC ABV70707;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 8493.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 271; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

```
  Query Match             30.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 2.2e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          13 GTACAGGGAG 22
               || |||||||
Db          10 GTTCAGGGAG 1
```

RESULT 428
ABV70046/c
ID ABV70046 standard; cDNA; 11 BP.
XX
AC ABV70046;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 7832.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 249; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically

CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 18 GGGAGTCCAG 27
||||||| ||
Db 11 GGGAGTCAAG 2

RESULT 429
ABK99385
ID ABK99385 standard; DNA; 11 BP.
XX
AC ABK99385;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human CYP3A5 gene polymorphic reference DNA sequence #20.
XX
KW Human; CYP3A5; polymorphism; cancer; cardiovascular disease; diabetes;
KW AIDS; African American; forensic marker; pharmacological; cytostatic;
KW antidiabetic; anti-HIV; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200253775-A2.
XX
PD 11-JUL-2002.
XX
PF 21-DEC-2001; 2001WO-EP015290.
XX
PR 28-DEC-2000; 2000EP-00128627.
PR 28-DEC-2000; 2000US-0258684P.
PR 29-DEC-2000; 2000US-0258952P.
PR 16-JAN-2001; 2001EP-00100172.
PR 18-JAN-2001; 2001US-0262859P.
PR 16-AUG-2001; 2001EP-00118884.
PR 16-AUG-2001; 2001US-0312825P.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Wojnowski L, Haberl M, Hustert E;
XX
DR WPI; 2002-583628/62.
XX
PT Novel CYP3A5 polynucleotide useful for diagnosis and treatment of cancer,
PT cardiovascular diseases, diabetes and AIDS, and for identifying
PT polymorphisms.
XX
PS Example 2; Page 49; 138pp; English.
XX
CC The present invention relates to a new CYP3A5 polynucleotide encoding a
CC polypeptide, where the polynucleotide is capable of hybridising to a
CC CYP3A5 gene. The invention is useful in an in vitro method for
CC identifying a polymorphism. The invention is also useful for useful for
CC diagnosing a disorder related to the presence of a molecular variant of a
CC CYP3A5 or susceptibility to such a disorder, where the disorder is
CC cancer, or diseases including cardiovascular diseases, diabetes and AIDS.
CC The invention can further be used for the preparation of a diagnostic
CC composition for diagnosing a disease in a subject having a genome
CC comprising a variant allele of the CYP3A5 gene, where the subject is an
CC African American. The molecules of the invention are as forensic markers
CC and in pharmacological studies. The present nucleic acid sequence
CC represents a human CYP3A5 gene polymorphism reference DNA sequence, as
CC described in the invention
XX
SQ Sequence 11 BP; 4 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 GTACAGGGAG 22
||||||| ||
Db 1 GTACAGGAAG 10

RESULT 430
ADE27824/c
ID ADE27824 standard; DNA; 11 BP.
XX
AC ADE27824;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human B7-2 mRNA targeted oligonucleotide SEQ ID 86.
XX
KW ss; human; B7-2; inflammatory skin disorder; antisense; psoriasis;
KW contact dermatitis; atopic dermatitis; seborrheic dermatitis;
KW nummular dermatitis; generalised exfoliative dermatitis; eczema;
KW critical costimulatory molecule.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003176374-A1.
XX
PD 18-SEP-2003.
XX
PF 09-MAY-2001; 2001US-00851871.
XX
PR 31-DEC-1996; 96US-00777266.
PR 04-JUN-1999; 99US-00326186.
PR 25-MAY-2000; 2000WO-US014471.
XX
PA (BENN/) BENNETT C F.
PA (VICK/) VICKERS T A.
PA (KARR/) KARRAS J G.
XX
PI Bennett CF, Vickers TA, Karras JG;
XX
DR WPI; 2003-863863/80.
XX
PT Treating an inflammatory skin disorder such as psoriasis comprises
PT topically applying an antisense compound targeted to the nucleic acid
PT encoding human B7 protein.
XX
PS Example 1; SEQ ID NO 86; 88pp; English.
XX
CC The invention relates to a method of treating an inflammatory skin
CC disorder in an individual by topically applying an antisense compound
CC targeted to a nucleic acid molecule encoding a human B7 protein. The
CC invention is for treating an inflammatory skin disorder in individual.
CC The skin disorder is psoriasis, contact dermatitis, atopic dermatitis,
CC seborrheic dermatitis, nummular dermatitis, generalised exfoliative
CC dermatitis or eczema. The invention effectively modulates critical
CC costimulatory molecules such as the B7 protein. The present sequence
CC represents a human B7-2 targeted oligonucleotide.
XX
SQ Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;

```
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          13 GTACAGGGAG 22
               |||| |||||
Db          11 GTACGGGGAG 2


RESULT 431
AAQ52961
ID   AAQ52961 standard; RNA; 12 BP.
XX
AC   AAQ52961;
XX
DT   25-MAR-2003  (revised)
DT   26-MAY-1994  (first entry)
XX
DE   Herpes simplex virus target sequence 39.
XX
KW   RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; HnRNA;
KW   picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;
KW   papilloma virus; HPV; Epstein-Barr virus; EBV; TCLV;
KW   T-cell leukaemia virus; hepatitis C virus; HCV; cytomegalovirus;
KW   influenza virus; HSV; herpes simplex virus; vector; immune response;
KW   antibody; ribozyme; viral RNA; treatment; ss.
XX
OS   Synthetic.
XX
PN   WO9323569-A1.
XX
PD   25-NOV-1993.
XX
PF   29-APR-1993;   93WO-US004020.
XX
PR   11-MAY-1992;   92US-00882689.
PR   14-MAY-1992;   92US-00882712.
PR   14-MAY-1992;   92US-00882713.
PR   14-MAY-1992;   92US-00882714.
PR   14-MAY-1992;   92US-00882823.
PR   14-MAY-1992;   92US-00882824.
PR   14-MAY-1992;   92US-00882886.
PR   14-MAY-1992;   92US-00882888.
PR   14-MAY-1992;   92US-00882889.
PR   14-MAY-1992;   92US-00882921.
PR   14-MAY-1992;   92US-00882922.
PR   14-MAY-1992;   92US-00883823.
PR   14-MAY-1992;   92US-00883849.
PR   14-MAY-1992;   92US-00884073.
PR   14-MAY-1992;   92US-00884074.
PR   14-MAY-1992;   92US-00884333.
PR   14-MAY-1992;   92US-00884422.
PR   14-MAY-1992;   92US-00884431.
PR   14-MAY-1992;   92US-00884436.
PR   14-MAY-1992;   92US-00884521.
PR   31-JUL-1992;   92US-00923738.
PR   26-AUG-1992;   92US-00935854.
PR   26-AUG-1992;   92US-00936086.
PR   18-SEP-1992;   92US-00948359.
PR   15-OCT-1992;   92US-00963322.
PR   07-DEC-1992;   92US-00987129.
PR   07-DEC-1992;   92US-00987130.
PR   07-DEC-1992;   92US-00987133.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Draper KG,  Dudycz LW,  Mcswiggen JA,  Macejak DG,  Holecek JJ;
PI   Mamone JA;
XX
DR   WPI; 1993-386599/48.
XX
PT   Enzymatic RNA molecules - used to inhibit viral replication, infection
PT   and gene expression.
XX
PS   Claim 5; Fig 15; 287pp; English.
XX
CC   The sequences (AAQ52923-Q53037) are pref. herpes simplex virus target
CC   sequences for enzymatic RNA molecules. The RNA molecules are
CC   complementary to a substrate binding region in the specified gene target.
CC   They also have enzymatic activity, in that they specifically cleave RNA
CC   in the target. The ERMs interfere with viral replication and therefore
CC   have anti-viral properties. They can be used to attenuate viruses to be
CC   used in vaccines. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC   on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct
CC   PI field.)
XX
SQ   Sequence 12 BP; 1 A; 5 C; 4 G; 0 T; 2 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   70.0%;  Pred. No. 2.5e+02;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           5 CCCTACGTGT 14
               ||| |||:|:
Db           1 CCCGACGUGU 10


RESULT 432
AAX79383/c
ID   AAX79383 standard; DNA; 12 BP.
XX
AC   AAX79383;
XX
DT   17-AUG-1999  (first entry)
XX
DE   HLA-DR typing probe F67.
XX
KW   Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;
KW   major histocompatibility complex; bone marrow transplant; primer;
KW   amplification; polymerase chain reaction; probe; polymorphism;
KW   sequence-specific oligonucleotide probe hybridisation; ss.
XX
OS   Synthetic.
XX
PN   US5468611-A.
XX
PD   21-NOV-1995.
XX
PF   08-APR-1993;   93US-00045530.
XX
PR   27-JUN-1990;   90US-00544218.
XX
PA   (BLOO-) BLOOD CENT RES FOUND INC.
XX
PI   Gorski JA,  Baxter-Lowe LA;
XX
DR   WPI; 1996-010091/01.
XX
PT   Improved method for HLA typing - by DNA amplification and sequence-
PT   specific oligo:nucleotide hybridisation, used to select bone marrow
PT   donors.
XX
PS   Disclosure; Col 19-20; 20pp; English.
XX
CC   A novel method of typing the human leukocyte antigen (HLA) of the major
CC   histocompatibility complex (MHC), esp. for typing donors for bone marrow
CC   transplants, involves determining if the donor tissue HLA-DR alleles are
CC   selected from the gp.: HLA-DRW52C, DR12a,b, DR3a,n, DR5a-e, DRNew1, DR6a,
CC   DR8a-d, DRW53a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and DR1a-
CC   c. The method uses PCR to amplify these regions followed by sequence-
CC   specific oligonucleotide probe hybridisation (SSOPH) using the probes
CC   AAX79365-X79429. SSOPH allows detection of polymorphisms that predict
CC   differences at a single amino acid level thus reducing errors and
CC   improving the chance of successfully matching tissues
XX
SQ   Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
```

```
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         16 CAGGGAGTCC 25
              |||| |||||
Db         12 CAGGAAGTCC 3


RESULT 433
AAT11933/c
ID   AAT11933 standard; DNA; 12 BP.
XX
AC   AAT11933;
XX
DT   13-JUL-1996  (first entry)
XX
DE   Antisense DNA to inhibit isoprenyl protein transferase expression.
XX
KW   isoprenyl protein transferase; farnesyl; geranyl geranyl; prenylation;
KW   inhibition; abnormal; uncontrolled; cell proliferation; cancer;
KW   cardiovascular disease; treatment; ss.
XX
OS   Synthetic.
XX
PN   GB2290791-A.
XX
PD   10-JAN-1996.
XX
PF   29-JUN-1995;   95GB-00013246.
XX
PR   29-JUN-1994;   94GB-00013035.
XX
PA   (SCRC ) SCRAS SOC CONSEILS RECH APPL SCI.
XX
PI   Colote S,  Pirotzky E;
XX
DR   WPI; 1996-042231/05.
XX
PT   Anti-sense oligo-nucleotide(s) hybridising to isoprenyl protein
PT   transferase genes - or their transcripts, for treating abnormal or
PT   uncontrolled cell proliferation e.g. cancer.
XX
PS   Claim 2; Page 20; 27pp; English.
XX
CC   AAT11906-41 are antisense oligonucleotides that are selectively
CC   hybridisable with a gene or the transcription products for sub-units of
CC   isoprenyl protein transferases, pref. farnesyl protein transferase or a
CC   gerany geranyl protein transferase. Oligonucleotides contg. these
CC   antisense sequences or their derivs. are useful in human or veterinary
CC   medicine for treatment of abnormal and/or uncontrolled cell
CC   proliferation, e.g. in cases of cardiovascular disease, cancer, viral
CC   infections or dermatology. Inhibiting prenylation prevents proteins from
CC   binding to active sites on cell membranes, so prevents transduction of
CC   extracellular cell signals and thus cell proliferation
XX
SQ   Sequence 12 BP; 1 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 ACGTGTACAG 18
              ||| ||||||
Db         11 ACGAGTACAG 2


RESULT 434
AAV48048/c
ID   AAV48048 standard; DNA; 12 BP.
XX
AC   AAV48048;
XX
DT   19-OCT-1998  (first entry)
XX
DE   Human B7-2 targetted oligonucleotide 10993.
XX
KW   ss; human; B7; T cell; inflammation; autoimmune disease; cell activation;
KW   cell proliferation.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .12
FT                   /*tag=  a
FT                   /note= "Phosphorothioate linkages"
XX
PN   WO9829124-A1.
XX
PD   09-JUL-1998.
XX
PF   16-DEC-1997;   97WO-US023270.
XX
PR   31-DEC-1996;   96US-00777266.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Vickers TA;
XX
DR   WPI; 1998-387783/33.
XX
PT   New oligo:nucleotide(s) that modulate expression of B7 proteins - used
PT   for, e.g. controlling activation and proliferation of T cells,
PT   particularly for treatment, diagnosis and prevention of inflammation.
XX
PS   Example 1; Page 39; 120pp; English.
XX
CC   The oligonucleotides which specifically hybridise to B7 modulate its
CC   expression (and thus T cell activation and proliferation). This is
CC   particularly useful for treatment and prevention of inflammation and
CC   autoimmune diseases, e.g. asthma, (juvenile) diabetes, myasthenia gravis,
CC   Grave's disease, rheumatoid arthritis, allograft rejection, psoriasis,
CC   (systemic) lupus erythematosus, multiple sclerosis, contact dermatitis,
CC   rhinitis, allergy, cancer and metastases. The oligonucleotides may also
CC   be used to manipulate T cell activation ex vivo; to determine or detect
CC   B7 protein expression; for diagnosis; as assay and purification reagents,
CC   and to study physiological roles of B7 proteins
XX
SQ   Sequence 12 BP; 2 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAG 22
              |||| |||||
Db         12 GTACGGGGAG 3


RESULT 435
AAV16579/c
ID   AAV16579 standard; DNA; 12 BP.
XX
AC   AAV16579;
XX
DT   12-JUN-1998  (first entry)
XX
DE   Probe F67 used to identify HLA-DR sequences.
XX
KW   DR region; major histocompatibility complex; HLA-DR; HLA-typing;
KW   HLA-DR beta consensus sequence; allelic polymorphism;
KW   HLA-DR beta-allelic polymorphism; probe; bone marrow; transplant; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
```

PN US5702885-A.
XX
PD 30-DEC-1997.
XX
PF 08-APR-1993; 93US-00057957.
XX
PR 27-JUN-1990; 90US-00544218.
XX
PA (BLOO-) BLOOD CENT RES FOUND INC.
XX
PI Gorski JA, Baxter-Lowe LA;
XX
DR WPI; 1998-076408/07.
XX
PT Oligo:nucleotide probes and primers and methods for HLA typing -
PT particularly for tissue typing for bone marrow transplants.
XX
PS Disclosure; Col 19; 20pp; English.
XX
CC Probes AAV16561-624 are used to identify differences in the DR region of
CC human major histocompatibility complex (HLA-DR). The specification
CC describes a method for HLA-typing, which includes an oligonucleotide
CC probe which undergoes sequence-specific hybridisation with an HLA-DR beta
CC consensus sequence at positions 61-64. The probe contains a labelling
CC substance other than a nucleotide sequence, which facilitates detection
CC of the probe. The HLA sequence of a subject is PCR amplified, and a probe
CC that recognises an allelic polymorphism at a selected HLA locus is
CC contacted with the amplified product. This first probe recognises a HLA-
CC DR beta-allelic polymorphism. A second (different) probe is brought into
CC contact with a second sample of the amplified DNA in a separate reaction,
CC and hybridisation detected. The probes and primers are used for HLA
CC typing, e.g. for tissue, especially bone marrow, transplants
XX
SQ Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 16 CAGGGAGTCC 25
|||| |||||
Db 12 CAGGAAGTCC 3

RESULT 436
AAZ41746/c
ID AAZ41746 standard; DNA; 12 BP.
XX
AC AAZ41746;
XX
DT 20-MAR-2003 (revised)
DT 21-JAN-2000 (first entry)
XX
DE Organic material detecting primer 107.
XX
KW Amplification; polymerase chain reaction; PCR; microorganism; compost;
KW detection; pollutant; soil; food; agricultural chemical; polymer;
KW organochlorine; primer; ss.
XX
OS Synthetic.
XX
PN DE19914461-A1.
XX
PD 21-OCT-1999.
XX
PF 30-MAR-1999; 99DE-01014461.
XX
PR 31-MAR-1998; 98JP-00087651.
PR 16-MAR-1999; 99JP-00069694.
XX
PA (SAOL) SANYO ELECTRIC CO LTD.
PA (NORQ) SOC TECHNO-INNOVATION AGRIC FORESTY & FI.
XX
PI Inoue T;
XX
DR WPI; 1999-592157/51.
XX
PT Novel polymerase chain reaction method, for differentiating between
PT microorganisms and for detecting contaminants.
XX
PS Example 1; Page 19; 78pp; German.
XX
CC This invention describes a novel method for the amplification of DNA
CC comprising (i) preparing many primers (P) with different probabilities of
CC amplification and (ii) simultaneous polymerase chain reaction (PCR) of
CC many different DNA using these primers. The method is used (i) to
CC differentiate between different microorganisms in a mixed population and
CC (ii) to determine presence/absence of an impurity (pollutant), or its
CC concentration, in e.g. soil, foods, compost etc., typically metals,
CC agricultural chemicals, polymers, organochlorine compounds etc. A
CC particular use is monitoring composting of organic material.
CC Amplification with many primers produces a lot of information, so
CC reliability of the test is improved, and many samples may be tested
CC quickly. AAZ41640-Z41855 represent the primers described in the method of
CC the invention. (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ Sequence 12 BP; 5 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 CTACGTGTAC 16
|| |||||||
Db 12 CTTCGTGTAC 3

RESULT 437
AAZ41530/c
ID AAZ41530 standard; DNA; 12 BP.
XX
AC AAZ41530;
XX
DT 19-JAN-2000 (first entry)
XX
DE Microbe detection in organic waste arbitrarily primed PCR primer #107.
XX
KW Microbe; detection; organic waste; arbitrarily primer PCR;
KW random amplified polymorphic DNA; amplification; PCR primer; ss.
XX
OS Synthetic.
XX
PN JP11276176-A.
XX
PD 12-OCT-1999.
XX
PF 31-MAR-1998; 98JP-00087652.
XX
PR 31-MAR-1998; 98JP-00087652.
XX
PA (SAOL) SANYO ELECTRIC CO LTD.
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
DR WPI; 1999-626940/54.
XX
PT Amplification of a DNA fragment - in order to establish the state of
PT existence of a microbe.
XX
PS Claim 1; Page 9; 40pp; Japanese.
XX
CC A method has been developed for the amplification of a DNA fragment in
CC which amplification is carried out on the DNA fragments of a number of
CC different DNAs. The method comprises a PCR reaction repeatedly carrying
CC out a heat-denaturing step, a primer annealing step and a polymerase
CC extending step, to amplify the DNA fragments of a plural of different
CC DNAs. The method can detect the existence of a microbe in organic waste.

```
CC   AAZ41424 to AAZ41639 represent PCR primers used in random amplified
CC   polymorphic DNA arbitrarily primed PCR, for the detection of microbes in
CC   organic waste
XX
SQ   Sequence 12 BP; 5 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTAC 16
              || |||||||
Db         12 CTTCGTGTAC 3


RESULT 438
AAA52398
ID   AAA52398 standard; DNA; 12 BP.
XX
AC   AAA52398;
XX
DT   18-SEP-2000  (first entry)
XX
DE   TdT-expressing Ramos cell VH deletion mutation, F66.
XX
KW   Lymphoid cell; antibody producing cell; Ramos cell; immunoglobulin M;
KW   IgM; V gene diversity; directed constitutive hypermutation;
KW   target sequence diversification; terminal deoxynucleotidyl transferase;
KW   TdT; clonal expansion; selection; heavy chain variable region; VH;
KW   mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200022111-A1.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-GB003358.
XX
PR   09-OCT-1998;   98GB-00022104.
PR   19-JAN-1999;   99GB-00001141.
PR   09-JUN-1999;   99GB-00013435.
XX
PA   (MEDI-) MEDICAL RES COUNCIL.
XX
PI   Sale JE,  Neuberger MS,  Cumbers SJ;
XX
DR   WPI; 2000-317971/27.
XX
PT   Lymphoid cell line preparation useful for producing gene products having
PT   desired activity, involves screening and selecting cells having ongoing
PT   target sequence diversification and higher mutation rates.
XX
PS   Example 4; Fig 6; 69pp; English.
XX
CC   The invention relates to a method of preparing a lymphoid cell line
CC   capable of capable of directed constitutive hypermutation of a target
CC   nucleic acid region. The method comprises screening a cell population for
CC   ongoing target sequence diversification and selecting a cell in which the
CC   rate of target nucleic acid mutation exceeds that of other nucleic acid
CC   mutation by a factor of 100 or more. The invention also relates to a
CC   method for preparing a gene product with a desired activity, comprising
CC   expressing a nucleic acid encoding the target gene operably linked to a
CC   sequence which directs hypermutation e.g., terminal deoxynucleotidyl
CC   transferase (TdT), in the lymphoid cell line, and identifying a cell or
CC   cells which express a mutated gene product with the desired activity. One
CC   or more clonal populations of the identified cells is established, and
CC   cells with an improved activity of interest are selected. These steps may
CC   be iteratively repeated until a gene product with a desired of activity
CC   is obtained. The cell lines prepared according to the method of the
CC   invention are used for directed constitutive hypermutation of a nucleic
CC   acid region in the preparation of a gene product, preferably an enzyme or
CC   an immunoglobulin (Ig) with a desired activity. In the exemplifications
CC   of the invention, IgM-secreting Ramos cells were selected for use as they
CC   undergo hypermutation during clonal expansion. This was determined on the
CC   basis of the amount of diversity in the heavy chain variable region (VH).
CC   Sequences AAA52366-A52434 represent fragments of Ramos cell VH region DNA
CC   containing mutations other than single nucleotide substitutions. The
CC   number assigned to the mutation represents the position in the wild-type
CC   VH DNA (AAA52364) to which the first nucleotide in the mutant fragment
CC   corresponds. Sequences AAA52388-A52434 represent mutations that occur in
CC   Ramos cells which express TdT, and sequences AAA52366-A52487 represent
CC   mutations that occur in non-TdT- expressing control Ramos cells
XX
SQ   Sequence 12 BP; 2 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGT 23
              | ||||||||
Db          2 TTCAGGGAGT 11


RESULT 439
AAF32890/c
ID   AAF32890 standard; DNA; 12 BP.
XX
AC   AAF32890;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Human B7-2 mRNA antisense oligonucleotide SEQ ID NO: 87.
XX
KW   Human; mouse; B7-1; B7-2; antisense; PCR primer; inflammation;
KW   autoimmune disorder; phosphorothioate backbone; ss.
XX
OS   Homo sapiens.
XX
PN   WO200074687-A1.
XX
PD   14-DEC-2000.
XX
PF   25-MAY-2000; 2000WO-US014471.
XX
PR   04-JUN-1999;   99US-00326186.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Vickers TA,  Karras JG;
XX
DR   WPI; 2001-049991/06.
XX
PT   Novel compound for diagnosing, preventing and treating immune disorders,
PT   comprising an oligonucleotide that specifically hybridizes with a nucleic
PT   acid sequence encoding B7 protein.
XX
PS   Example 1; Page 51; 162pp; English.
XX
CC   The present invention provides sequences of antisense oligonucleotides
CC   targeted at the murine and human B7-1 and B7-2 coding and mRNA sequences.
CC   The antisense sequences have phosphorothioate backbones and some
CC   nucleotides are 2'-methoxyethoxy residues. The sequences can be used in
CC   the treatment of inflammatory and autoimmune disorders, including asthma,
CC   juvenile diabetes mellitus, myasthenia gravis, Graves' disease,
CC   rheumatoid arthritis, allograft rejection, inflammatory bowel disease,
CC   multiple sclerosis, psoriasis, systemic lupus erythematosus, contact
CC   dermatitis, rhinitis, allergies and cancer
XX
SQ   Sequence 12 BP; 2 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          13 GTACAGGGAG 22
               |||| |||||
Db          12 GTACGGGGAG 3
```

RESULT 440
AAC97881/c
ID AAC97881 standard; DNA; 12 BP.
XX
AC AAC97881;
XX
DT 28-FEB-2001 (first entry)
XX
DE Primer used to illustrate DNA amplification method SEQ ID 107.
XX
KW Primer; amplification; selective; ss.
XX
OS Synthetic.
XX
PN JP2000270867-A.
XX
PD 03-OCT-2000.
XX
PF 19-MAR-1999; 99JP-00076844.
XX
PR 19-MAR-1999; 99JP-00076844.
XX
PA (SAOL) SANYO ELECTRIC CO LTD.
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
DR WPI; 2001-011047/02.
XX
PT Amplification of a DNA fragment and its apparatus.
XX
PS Example 1; Page 9; 32pp; Japanese.
XX
CC This invention relates to a method for amplifying a DNA fragment. The
CC method comprises successive repetitions of heat-denaturing, annealing of
CC a primer and an extending step using a DNA polymerase. The method makes
CC use of a cDNA pool in which the primer is one primer or a pair of primer
CC sets and has an amplification probability which allows it to amplify a
CC DNA fragment from a limited number of the cDNAs among the DNA pool (where
CC the limited number is in the range of 1 to 25). Also included in the
CC invention are apparatus used for carrying out the method, a primer and a
CC DNA polymerase and a kit used for amplifying a DNA fragment. The method
CC can be used to amplify a limited number of cDNAs from a pool in which a
CC wide variety of cDNAs are present. Oligonucleotides AAC97775 - AAC97990
CC represent primers used in an example illustrating the method of the
CC invention
XX
SQ Sequence 12 BP; 5 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match   30.0%; Score 8.4; DB 1; Length 12;
  Best Local Similarity   90.0%; Pred. No. 2.5e+02;
  Matches   9; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

```
Qy           7 CTACGTGTAC 16
               || |||||||
Db          12 CTTCGTGTAC 3
```

RESULT 441
ABH94723/c
ID ABH94723 standard; DNA; 12 BP.
XX
AC ABH94723;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 294716 for detecting SNP TSC0016238.
XX
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 294716; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 1 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match   30.0%; Score 8.4; DB 1; Length 12;
  Best Local Similarity   90.0%; Pred. No. 2.5e+02;
  Matches   9; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

```
Qy           8 TACGTGTACA 17
               ||||| ||||
Db          12 TACGTATACA 3
```

RESULT 442
ABI06355
ID ABI06355 standard; DNA; 12 BP.
XX
AC ABI06355;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 306328 for detecting SNP TSC0021949.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardicvascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX

```
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 306328; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGT 23
              || |||||||
Db          1 TAGAGGGAGT 10


RESULT 443
ABI07028/c
ID   ABI07028 standard; DNA; 12 BP.
XX
AC   ABI07028;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 307001 for detecting SNP TSC0022291.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 307001; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 8 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGG 20
              ||||| ||||
Db         10 GTGTAGAGGG 1


RESULT 444
ABH73958
ID   ABH73958 standard; DNA; 12 BP.
XX
AC   ABH73958;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 273943 for detecting SNP TSC0003372.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 273943; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
```

```
  Query Match           30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGT 23
              || |||||||
Db          2 TAGAGGGAGT 11


RESULT 445
ABI24391
ID   ABI24391 standard; DNA; 12 BP.
XX
AC   ABI24391;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 324364 for detecting SNP TSC0031975.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 324364; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 1 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAG 22
              |||| |||||
Db          1 GTACGGGGAG 10


RESULT 446
ABI63508
ID   ABI63508 standard; DNA; 12 BP.
XX
AC   ABI63508;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 363481 for detecting SNP TSC0053879.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 363481; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 GTGTACAGGG 20
              ||||| ||||
Db          1 GTGTAAAGGG 10


RESULT 447
ABI22910
ID   ABI22910 standard; DNA; 12 BP.
XX
AC   ABI22910;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 322883 for detecting SNP TSC0031094.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
```

```
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 322883; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAG 22
              ||| ||||||
Db          2 GTAGAGGGAG 11


RESULT 448
ABI25222
ID   ABI25222 standard; DNA; 12 BP.
XX
AC   ABI25222;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 325195 for detecting SNP TSC0032450.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 325195; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGT 23
              || |||||||
Db          1 TAGAGGGAGT 10


RESULT 449
ABH76574
ID   ABH76574 standard; DNA; 12 BP.
XX
AC   ABH76574;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 276567 for detecting SNP TSC0004226.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 276567; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
```

```
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGT 23
              || |||||||
Db          2 TATAGGGAGT 11


RESULT 450
ABH87306/c
ID   ABH87306 standard; DNA; 12 BP.
XX
AC   ABH87306;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 287299 for detecting SNP TSC0013035.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 287299; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTA 15
              ||||||| ||
Db         12 CCTACGTATA 3


RESULT 451
ABH71336/c
ID   ABH71336 standard; DNA; 12 BP.
XX
AC   ABH71336;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 271313 for detecting SNP TSC0002462.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 271313; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGT 23
              || |||||||
Db         11 TAAAGGGAGT 2


RESULT 452
ABI35820
ID   ABI35820 standard; DNA; 12 BP.
XX
AC   ABI35820;
XX
DT   22-FEB-2002  (first entry)
XX
```

```
DE   Oligonucleotide primer SEQ ID NO 335793 for detecting SNP TSC0039015.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 335793; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGA 21
               |||| |||||
Db           1 TGTAGAGGGA 10


RESULT 453
ABI65800
ID   ABI65800 standard; DNA; 12 BP.
XX
AC   ABI65800;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 365773 for detecting SNP TSC0055324.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 365773; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          12 TGTACAGGGA 21
               |||| |||||
Db           3 TGTATAGGGA 12


RESULT 454
ABH85342/c
ID   ABH85342 standard; DNA; 12 BP.
XX
AC   ABH85342;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 285335 for detecting SNP TSC0012245.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
```

```
PS   Claim 1; SEQ ID NO 285335; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 2 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACA 17
              ||||||||| |
Db         11 TACGTGTATA 2


RESULT 455
ABH98134
ID   ABH98134 standard; DNA; 12 BP.
XX
AC   ABH98134;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 298127 for detecting SNP TSC0017923.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 298127; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGA 21
              |||| |||||
Db          3 TGTAAAGGGA 12


RESULT 456
ABH79179/c
ID   ABH79179 standard; DNA; 12 BP.
XX
AC   ABH79179;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 279172 for detecting SNP TSC0007003.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 279172; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGA 21
              |||| |||||
Db         12 TGTATAGGGA 3
```

```
RESULT 457
ABI77362/c
ID   ABI77362 standard; DNA; 12 BP.
XX
AC   ABI77362;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 377335 for detecting SNP TSC0062277.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 377335; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 1 A; 6 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAG 22
              ||| ||||||
Db         11 GTAGAGGGAG 2


RESULT 458
ABI65126/c
ID   ABI65126 standard; DNA; 12 BP.
XX
AC   ABI65126;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 365099 for detecting SNP TSC0054913.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 365099; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 6 A; 2 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match           30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACA 17
              |||||||| |
Db         12 TACGTGTATA 3


RESULT 459
ABI16276
ID   ABI16276 standard; DNA; 12 BP.
XX
AC   ABI16276;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 316249 for detecting SNP TSC0027355.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
```

```
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 316249; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGT 23
               || |||||||
Db          2 TATAGGGAGT 11


RESULT 460
ABI22691
ID   ABI22691 standard; DNA; 12 BP.
XX
AC   ABI22691;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 322664 for detecting SNP TSC0030993.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 322664; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 TACAGGGAGT 23
               || |||||||
Db          1 TAAAGGGAGT 10


RESULT 461
ABI06949/c
ID   ABI06949 standard; DNA; 12 BP.
XX
AC   ABI06949;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 306922 for detecting SNP TSC0022248.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 306922; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 5 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
```

```
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         13 GTACAGGGAG 22
              ||| ||||||
Db         10 GTATAGGGAG 1


RESULT 462
ABI25808/c
ID   ABI25808 standard; DNA; 12 BP.
XX
AC   ABI25808;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 325781 for detecting SNP TSC0032711.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 325781; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGA 21
              |||| |||||
Db         10 TGTATAGGGA 1


RESULT 463
ABI30071
ID   ABI30071 standard; DNA; 12 BP.
XX
AC   ABI30071;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 330044 for detecting SNP TSC0035293.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 330044; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGA 21
              |||| |||||
Db          3 TGTAGAGGGA 12


RESULT 464
ABI10705
ID   ABI10705 standard; DNA; 12 BP.
XX
AC   ABI10705;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 310678 for detecting SNP TSC0024049.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
```

PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 310678; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

```
  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CCTACGTGTA 15
              |||||| |||
Db          2 CCTACGCGTA 11
```

RESULT 465
ABI37238
ID ABI37238 standard; DNA; 12 BP.
XX
AC ABI37238;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 337211 for detecting SNP TSC0039735.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 337211; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 1 C; 2 G; 6 T; 0 U; 0 Other;

```
  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACA 17
              |||||||| |
Db          3 TACGTGTATA 12
```

RESULT 466
ABI51683/c
ID ABI51683 standard; DNA; 12 BP.
XX
AC ABI51683;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 351656 for detecting SNP TSC0047427.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 351656; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

```
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGG 19
              |||||| |||
Db         12 CGTGTAAAGG 3


RESULT 467
ABH74522/c
ID   ABH74522 standard; DNA; 12 BP.
XX
AC   ABH74522;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 274507 for detecting SNP TSC0003575.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 274507; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         12 TGTACAGGGA 21
              |||| |||||
Db         10 TGTAGAGGGA 1


RESULT 468
ABH85340/c
ID   ABH85340 standard; DNA; 12 BP.
XX
AC   ABH85340;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 285333 for detecting SNP TSC0012245.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 285333; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 1 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             30.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TACGTGTACA 17
              ||||| ||||
Db         12 TACGTATACA 3


RESULT 469
AAF92639/c
ID   AAF92639 standard; DNA; 12 BP.
XX
AC   AAF92639;
XX
DT   16-MAY-2001  (first entry)
XX
DE   HLA-DR typing probe #19.
XX
```

KW Human; leukocyte antigen; HLA; typing; sequence specific probe; SSOPH;
KW ss.
XX
OS Homo sapiens.
XX
PN US6194147-B1.
XX
PD 27-FEB-2001.
XX
PF 30-DEC-1997; 97US-00000805.
XX
PR 27-JUN-1990; 90US-00544218.
PR 08-APR-1993; 93US-00057957.
XX
PA (BLOO-) BLOOD CENT RES FOUND INC.
XX
PI Baxter-Lowe LA, Gorski JA;
XX
DR WPI; 2001-217923/22.
XX
PT Human leukocyte antigen typing by amplifying a sample followed by
PT sequence specific oligonucleotide hybridization with labeled
PT oligonucleotide probes that hybridize with a series of known control DNA
PT sequences.
XX
PS Disclosure; Col 11-14; 16pp; English.
XX
CC The present invention relates to human leukocyte antigen (HLA) typing.
CC The method involves detecting polymorphic residues by sequence specific
CC oligonucleotide probe hybridization (SSOPH) with labeled oligonucleotide
CC probes
XX
SQ Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 16 CAGGGAGTCC 25
|||| |||||
Db 12 CAGGAAGTCC 3

RESULT 470
ABL59179/c
ID ABL59179 standard; DNA; 12 BP.
XX
AC ABL59179;
XX
DT 27-SEP-2002 (first entry)
XX
DE Oligonucleotide used to create plasmid pAG802 from plasmid pAG800.
XX
KW Glycopeptide; class II MHC molecule; CD4+ T-lymphocyte; cytokine;
KW immune response; antigen; vaccine; immunogen; microbial infection; ss.
XX
OS Synthetic.
XX
PN WO200250108-A2.
XX
PD 27-JUN-2002.
XX
PF 20-DEC-2001; 2001WO-FR004100.
XX
PR 21-DEC-2000; 2000FR-00016808.
XX
PA (INSP) INST PASTEUR.
XX
PI Marchal G, Romain F, Pescher P;
XX
DR WPI; 2002-519874/55.
XX
PT Immunogenic glycopeptides derived from pathogenic microorganisms, useful
PT for vaccination against or diagnosis of infections by microorganisms,
PT e.g. tuberculosis or candida.
XX
PS Example 3; Page 27; 58pp; French.
XX
CC The present sequence represents an oligonucleotide which was used to
CC create plasmid pAG802 from plasmid pAG800. This plasmid was used in the
CC course of the invention. The specification describes immunogenic
CC glycopeptides, which comprise a glycosylated T epitope of microbial
CC origin. At least one neutral amino acid is glycosidically bonded to a di-
CC or trisaccharide and at least 15% of the amino acids are proline (one of
CC which is in position -1 to -4 relative to the neutral amino acid).
CC Glycopeptides of the invention are expressed by a class II MHC molecule,
CC (specifically recognized by CD4+ T-lymphocytes induced by immunization
CC with the parent natural glycoprotein but not by CD4+ T-lymphocytes
CC induced by the analogous non-glycosylated peptide, and can induce
CC proliferation of the CD4+ T-lymphocytes by which they are recognized and
CC secretion of cytokines by these lymphocytes. The glycopeptides induce a
CC protective cellular immune response and optionally humoral immune
CC response, are completely non-pathogenic and can be used in
CC immunosuppressed patients. They have antigenic activity at least
CC equivalent to conventional antigens, have very high specificity and are
CC totally free of cross reactivity. Glycopeptides of the invention are used
CC in the production of immunogen or vaccine compositions. In particular,
CC they are useful for vaccination against, or diagnosis of, infections by
CC the pathogenic microorganisms
XX
SQ Sequence 12 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGCCCTACGT 12
||||| ||||
Db 12 GGCCCAACGT 3

RESULT 471
ADD68863
ID ADD68863 standard; DNA; 12 BP.
XX
AC ADD68863;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human low homology shuffling-related DNA.
XX
KW recombination; family gene shuffling; diversity; ds; low homology; gene.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .12
FT /*tag= a
FT /partial
FT /product= "Human low homology shuffling-related peptide"
FT /note= "No start or stop codon"
XX
PN US2003054390-A1.
XX
PD 20-MAR-2003.
XX
PF 15-JUL-2002; 2002US-00196473.
XX
PR 19-JAN-1999; 99US-0116447P.
PR 05-FEB-1999; 99US-0118813P.
PR 05-FEB-1999; 99US-0118854P.
PR 24-JUN-1999; 99US-0141049P.
PR 28-SEP-1999; 99US-00408392.
PR 12-OCT-1999; 99US-00416375.
PR 12-OCT-1999; 99US-00416837.
PR 18-JAN-2000; 2000US-00484850.

PR 18-JAN-2000; 2000US-00494282.
PR 21-NOV-2000; 2000US-00721601.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Crameri A, Stemmer WPC, Minshull J, Bass SH, Welch M, Ness JE;
PI Gustafsson C, Patten PA;
XX
DR WPI; 2003-777161/73.
DR P-PSDB; ADD68862.
XX
PT Recombining homologous nucleic acids for introducing nucleic acid family
PT diversity during nucleic acid recombination, by hybridizing a set of
PT family gene shuffling oligonucleotides, and elongating oligonucleotides.
XX
PS Disclosure; Fig 2; 31pp; English.
XX
CC The invention relates to a novel method for recombining homologous
CC nucleic acids comprising hybridising a set of family gene shuffling
CC oligonucleotides, elongating the set and hence providing a population of
CC recombined nucleic acids. The method of the invention may be useful for
CC recombining homologous nucleic acids and for introducing nucleic acid
CC family diversity during nucleic acid recombination. The method provides
CC substantially simplified shuffling protocols which can be used to produce
CC family shuffled nucleic acids without isolating or cloning full-length
CC homologous nucleic acids. Furthermore, the method may be used to
CC recombine homologous nucleic acids with low sequence similarity. The
CC current sequence is that of the human low homology shuffling-related DNA
CC of the invention.
XX
SQ Sequence 12 BP; 2 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 18 GGGAGTCCAG 27
||| ||||||
Db 2 GGGGGTCCAG 11

RESULT 472
ADE27825/c
ID ADE27825 standard; DNA; 12 BP.
XX
AC ADE27825;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human B7-2 mRNA targeted oligonucleotide SEQ ID 87.
XX
KW ss; human; B7-2; inflammatory skin disorder; antisense; psoriasis;
KW contact dermatitis; atopic dermatitis; seborrheic dermatitis;
KW nummular dermatitis; generalised exfoliative dermatitis; eczema;
KW critical costimulatory molecule.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003176374-A1.
XX
PD 18-SEP-2003.
XX
PF 09-MAY-2001; 2001US-00851871.
XX
PR 31-DEC-1996; 96US-00777266.
PR 04-JUN-1999; 99US-00326186.
PR 25-MAY-2000; 2000WO-US014471.
XX
PA (BENN/) BENNETT C F.
PA (VICK/) VICKERS T A.
PA (KARR/) KARRAS J G.
XX
PI Bennett CF, Vickers TA, Karras JG;
XX
DR WPI; 2003-863863/80.
XX
PT Treating an inflammatory skin disorder such as psoriasis comprises
PT topically applying an antisense compound targeted to the nucleic acid
PT encoding human B7 protein.
XX
PS Example 1; SEQ ID NO 87; 88pp; English.
XX
CC The invention relates to a method of treating an inflammatory skin
CC disorder in an individual by topically applying an antisense compound
CC targeted to a nucleic acid molecule encoding a human B7 protein. The
CC invention is for treating an inflammatory skin disorder in individual.
CC The skin disorder is psoriasis, contact dermatitis, atopic dermatitis,
CC seborrheic dermatitis, nummular dermatitis, generalised exfoliative
CC dermatitis or eczema. The invention effectively modulates critical
CC costimulatory molecules such as the B7 protein. The present sequence
CC represents a human B7-2 targeted oligonucleotide.
XX
SQ Sequence 12 BP; 2 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 GTACAGGGAG 22
|||| |||||
Db 12 GTACGGGGAG 3

RESULT 473
AAH74110/c
ID AAH74110 standard; DNA; 15 BP.
XX
AC AAH74110;
XX
DT 17-DEC-2001 (first entry)
XX
DE Primer #7 used in identification of gene transcripts.
XX
KW Primer; DGE; differential gene expression; gene identification; ss.
XX
OS Unidentified.
XX
PN EP1113382-A1.
XX
PD 04-JUL-2001.
XX
PF 27-DEC-1999; 99EP-00126017.
XX
PR 27-DEC-1999; 99EP-00126017.
XX
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI Colinge J, Feger G;
XX
DR WPI; 2001-443815/48.
XX
PT Identifying gene transcripts, involves generating first set of raw
PT sequences by sequencing biological material, isolating first ditags and
PT first tags, determining abundance of first tags, reducing sequencing
PT errors.
XX
PS Disclosure; Fig 10; 104pp; English.
XX
CC The invention relates to a method of identifying gene transcripts, which
CC involves generating at least a first set of raw sequences (RS) by
CC sequencing at least a first type of biological material, isolating first
CC ditags (DT) from RS, isolating first tags (T1) from DT, determining the
CC abundance of T1 and identifying T1, and then reducing the amount of
CC sequencing errors using a statistical model for sequencing errors to be
CC applied to T1. The method is useful for the identification of gene

CC transcripts such as RNA or their corresponding cDNAs, and also for
CC collecting information from several cell types, e.g. with reference to
CC DGE (differential gene expression) studies. The method has improved
CC efficiency in the treatment of errors, greatly reduces the error rate of
CC the tags by estimating the error rate and consequently rejecting
CC dangerous tags. It provides an easy way for consulting the identified
CC tags by use of an improved graphical interface. Sequencing error is
CC reduced by applying a statistical model. A measure of correctness of
CC identification is provided, by allowing the user to confirm the
CC identification through use of more than one database. The method provides
CC not only a text form which is richer than other interfaces for similar
CC data in terms of information about identified tags, but also an improved
CC graphical interface which allows an easy interpretation of the results
CC and an easy access to e.g. the KEGG (undefined) pathway. The present
CC sequence represents primer #7 used in the method of the invention
XX
SQ Sequence 15 BP; 5 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 29.3%; Score 8.2; DB 1; Length 15;
Best Local Similarity 76.9%; Pred. No. 3.7e+02;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CTACGTGTACAGG 19
|| | |||||| |
Db 13 CTTCCTGTACATG 1

RESULT 474
ABZ61654/c
ID ABZ61654 standard; RNA; 17 BP.
XX
AC ABZ61654;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human H-Ras DNAzyme target #445.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US016840.
XX
PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS Claim 58; Page 119; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC ribozymes of the invention
XX
SQ Sequence 17 BP; 5 A; 6 C; 5 G; 0 T; 1 U; 0 Other;

Query Match 29.3%; Score 8.2; DB 1; Length 17;
Best Local Similarity 76.9%; Pred. No. 4.2e+02;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CTACGTGTACAGG 19
|| | ||||| ||
Db 16 CTCCCTGTACTGG 4

RESULT 475
AAL62639
ID AAL62639 standard; DNA; 20 BP.
XX
AC AAL62639;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human CD36 antigen-like 1 (CD36L1) antisense oligo, ISIS 199306.
XX
KW Human; CD36 antigen-like 1; CD36L1; scavenger receptor class B type 1;
KW CLA-1; SRB1; SR-BI; cardiovascular; metabolic disorder; atherosclerosis;
KW lipid metabolism; gene therapy; phosphorothioate backbone; antisense; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidines are 5-
FT methylcytidines"
FT modified_base 1. .5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 16. .20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
XX
PN WO2003052062-A2.
XX
PD 26-JUN-2003.
XX
PF 09-DEC-2002; 2002WO-US039183.
XX
PR 18-DEC-2001; 2001US-00024396.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dobie KW;
XX
DR WPI; 2003-533006/50.
XX
PT New compound, having a sequence targeted to a nucleic acid encoding
PT CD36L1, useful for preparing a composition for treating
PT hyperproliferative or autoimmune disorders.
XX
PS Claim 3; Page 81; 122pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of class B scavenger receptor, CD36 antigen
CC -like 1 (CD36L1). CD36L1 is also known as scavenger receptor class B type
CC 1 (SRB1), CLA-1 and mouse homologue, SR-BI. The antisense compound is
CC useful for preparing a composition for treating metabolic or

```
CC   cardiovascular disorder, e.g. altered lipid metabolism or
CC   atherosclerosis. It is also used in gene therapy. The present sequence is
CC   an antisense oligonucleotide targetted to human CD36L1 DNA. This sequence
CC   is used to illustrate the method of the invention
XX
SQ   Sequence 20 BP; 3 A; 8 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             29.3%;  Score 8.2;  DB 1;  Length 20;
  Best Local Similarity   76.9%;  Pred. No. 4.7e+02;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 CGTGTACAGGGAG 22
              | |||||| | ||
Db          2 CCTGTACACGTAG 14


RESULT 476
AAL62640
ID   AAL62640 standard; DNA; 20 BP.
XX
AC   AAL62640;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human CD36 antigen-like 1 (CD36L1) antisense oligo, ISIS 199307.
XX
KW   Human; CD36 antigen-like 1; CD36L1; scavenger receptor class B type 1;
KW   CLA-1; SRB1; SR-BI; cardiovascular; metabolic disorder; atherosclerosis;
KW   lipid metabolism; gene therapy; phosphorothioate backbone; antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003052062-A2.
XX
PD   26-JUN-2003.
XX
PF   09-DEC-2002; 2002WO-US039183.
XX
PR   18-DEC-2001; 2001US-00024396.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Dobie KW;
XX
DR   WPI; 2003-533006/50.
XX
PT   New compound, having a sequence targeted to a nucleic acid encoding
PT   CD36L1, useful for preparing a composition for treating
PT   hyperproliferative or autoimmune disorders.
XX
PS   Claim 3; Page 81; 122pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of class B scavenger receptor, CD36 antigen
CC   -like 1 (CD36L1). CD36L1 is also known as scavenger receptor class B type
CC   1 (SRB1), CLA-1 and mouse homologue, SR-BI. The antisense compound is
CC   useful for preparing a composition for treating metabolic or
CC   cardiovascular disorder, e.g. altered lipid metabolism or
CC   atherosclerosis. It is also used in gene therapy. The present sequence is
CC   an antisense oligonucleotide targetted to human CD36L1 DNA. This sequence
CC   is used to illustrate the method of the invention
XX
SQ   Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             29.3%;  Score 8.2;  DB 1;  Length 20;
  Best Local Similarity   76.9%;  Pred. No. 4.7e+02;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGG 19
              || | ||||||
Db          7 CTCCCTGTACACG 19


RESULT 477
AAT17883/c
ID   AAT17883 standard; DNA; 21 BP.
XX
AC   AAT17883;
XX
DT   21-MAY-1996  (first entry)
XX
DE   IL-11 receptor alpha chain probe 489.
XX
KW   Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
KW   therapy; diagnosis; probe; ss.
XX
OS   Synthetic.
XX
PN   WO9607737-A1.
XX
PD   14-MAR-1996.
XX
PF   05-SEP-1995;   95WO-AU000578.
XX
PR   05-SEP-1994;   94AU-00007901.
PR   05-SEP-1994;   94AU-00007902.
XX
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI   Hilton DJ;
XX
DR   WPI; 1996-171612/17.
XX
PT   Nucleic acid encoding haemopoietin receptor containing conserved amino
PT   acid motif esp. IL-11 receptor alpha chain - used for developing IL-11
PT   (ant)agonists.
XX
PS   Example 3; Page 21; 87pp; English.
XX
CC   Probe 489 (AAT17883) was used to detect interleukin-11 (IL-11) receptor
CC   alpha chain sequences following RT-PCR amplification of RNA from 15
CC   primary tissue samples and 17 cell lines. Nr1 mRNA (see AAT17868) was
CC   detected in 3T3-L1 cells, the stromal line BAd, the embryonic carcinoma
CC   cell line PC13 and the factor-dependent haemopoietin cell lines FDCP-1
CC   and D35 expressed Nr1 mRNA. Positive primary tissues included bone
CC   marrow, spleen, thymus, liver, brain, heart kidney, muscle and salivary
CC   gland
XX
SQ   Sequence 21 BP; 3 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

  Query Match             29.3%;  Score 8.2;  DB 1;  Length 21;
  Best Local Similarity   76.9%;  Pred. No. 4.8e+02;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CTACGTGTACAGG 19
              || |  |||||||
Db         15 CTCCAAGTACAGG 3


RESULT 478
```

```
ABQ72155/c
ID   ABQ72155 standard; DNA; 9 BP.
XX
AC   ABQ72155;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Zinc finger protein related oligonucleotide target SEQ ID NO:2453.
XX
KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200242459-A2.
XX
PD   30-MAY-2002.
XX
PF   20-NOV-2001; 2001WO-US043438.
XX
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Liu Q;
XX
DR   WPI; 2002-500284/53.
XX
PT   New zinc finger protein that binds to target site, useful in studying
PT   gene function and for human therapeutics and plant engineering, comprises
PT   first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS   Example 1; Page 62; 81pp; English.
XX
CC   The present invention describes a zinc finger protein (I) that binds to a
CC   target site, comprising a first (F1), a second (F2), and a third (F3)
CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC   binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC   binds to the S2 target subsite, and selecting the F3 zinc finger such
CC   that it binds to the S3 target subsite, thus designing (I) that binds to
CC   a target site. (I) is useful for recognition of triplet target subsites
CC   having the nucleotide G in the 5'-most position of the subsite. (I) is
CC   useful in studying gene function, and for human therapeutics and plant
CC   engineering. (I), (II) or (III) is useful in therapeutic methods to
CC   modulate the expression of a target region within a subject, in
CC   diagnostic methods for sequence specific detection of target nucleic acid
CC   in a sample, and in assays to determined the phenotype and function of
CC   gene expression. (I) has improved affinity and specificity for their
CC   target sequences, as well as enhanced biological activity. ABQ71213 to
CC   ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC   finger peptides which are given in the exemplification of the present
CC   invention
XX
SQ   Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          9 CGGGCCCT 2


RESULT 479
ABQ71897
ID   ABQ71897 standard; DNA; 9 BP.
XX
AC   ABQ71897;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Zinc finger protein related oligonucleotide target SEQ ID NO:2195.
XX
KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200242459-A2.
XX
PD   30-MAY-2002.
XX
PF   20-NOV-2001; 2001WO-US043438.
XX
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Liu Q;
XX
DR   WPI; 2002-500284/53.
XX
PT   New zinc finger protein that binds to target site, useful in studying
PT   gene function and for human therapeutics and plant engineering, comprises
PT   first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS   Example 1; Page 57; 81pp; English.
XX
CC   The present invention describes a zinc finger protein (I) that binds to a
CC   target site, comprising a first (F1), a second (F2), and a third (F3)
CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC   binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC   binds to the S2 target subsite, and selecting the F3 zinc finger such
CC   that it binds to the S3 target subsite, thus designing (I) that binds to
CC   a target site. (I) is useful for recognition of triplet target subsites
CC   having the nucleotide G in the 5'-most position of the subsite. (I) is
CC   useful in studying gene function, and for human therapeutics and plant
CC   engineering. (I), (II) or (III) is useful in therapeutic methods to
CC   modulate the expression of a target region within a subject, in
CC   diagnostic methods for sequence specific detection of target nucleic acid
CC   in a sample, and in assays to determined the phenotype and function of
CC   gene expression. (I) has improved affinity and specificity for their
CC   target sequences, as well as enhanced biological activity. ABQ71213 to
CC   ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC   finger peptides which are given in the exemplification of the present
CC   invention
XX
SQ   Sequence 9 BP; 2 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTC 24
              ||||||||
Db          2 AGGGAGTC 9


RESULT 480
ABQ71800/c
ID   ABQ71800 standard; DNA; 9 BP.
XX
AC   ABQ71800;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Zinc finger protein related oligonucleotide target SEQ ID NO:2098.
```

XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US043438.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS Example 1; Page 55; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determined the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
SQ Sequence 9 BP; 2 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCCTACGT 12
||||||||
Db 9 CCCTACGT 2

RESULT 481
ABQ71802/c
ID ABQ71802 standard; DNA; 9 BP.
XX
AC ABQ71802;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2100.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US043438.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS Example 1; Page 55; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determined the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
SQ Sequence 9 BP; 2 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCCTACGT 12
||||||||
Db 9 CCCTACGT 2

RESULT 482
ABQ72156/c
ID ABQ72156 standard; DNA; 9 BP.
XX
AC ABQ72156;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2454.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX

```
PD   30-MAY-2002.
XX
PF   20-NOV-2001; 2001WO-US043438.
XX
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Liu Q;
XX
DR   WPI; 2002-500284/53.
XX
PT   New zinc finger protein that binds to target site, useful in studying
PT   gene function and for human therapeutics and plant engineering, comprises
PT   first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS   Example 1; Page 62; 81pp; English.
XX
CC   The present invention describes a zinc finger protein (I) that binds to a
CC   target site, comprising a first (F1), a second (F2), and a third (F3)
CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC   binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC   binds to the S2 target subsite, and selecting the F3 zinc finger such
CC   that it binds to the S3 target subsite, thus designing (I) that binds to
CC   a target site. (I) is useful for recognition of triplet target subsites
CC   having the nucleotide G in the 5'-most position of the subsite. (I) is
CC   useful in studying gene function, and for human therapeutics and plant
CC   engineering. (I), (II) or (III) is useful in therapeutic methods to
CC   modulate the expression of a target region within a subject, in
CC   diagnostic methods for sequence specific detection of target nucleic acid
CC   in a sample, and in assays to determined the phenotype and function of
CC   gene expression. (I) has improved affinity and specificity for their
CC   target sequences, as well as enhanced biological activity. ABQ71213 to
CC   ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC   finger peptides which are given in the exemplification of the present
CC   invention
XX
SQ   Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          9 CGGGCCCT 2


RESULT 483
ADA64224
ID   ADA64224 standard; DNA; 9 BP.
XX
AC   ADA64224;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Zinc finger target sequence DNA #682.
XX
KW   ds; target sequence; zinc finger protein;
KW   multi-finger zinc finger protein; improved affinity;
KW   improved specificity; enhanced biological activity.
XX
OS   Synthetic.
XX
PN   US2003068675-A1.
XX
PD   10-APR-2003.
XX
PF   20-NOV-2001; 2001US-00990186.
XX
PR   24-MAR-1999;   99US-0126238P.
PR   24-MAR-1999;   99US-0126239P.
PR   30-JUL-1999;   99US-0146595P.
PR   30-JUL-1999;   99US-0146615P.
PR   23-MAR-2000; 2000US-00535008.
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (LIUQ/) LIU Q.
XX
PI   Liu Q;
XX
DR   WPI; 2003-567233/53.
XX
PT   Designing zinc finger protein that has three zinc fingers from N-terminus
PT   and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT   site, by selecting zinc fingers that bind their respective subsites.
XX
PS   Disclosure; Page 23; 34pp; English.
XX
CC   The invention relates to a method of designing a zinc finger protein. The
CC   method is useful for designing a zinc finger protein. The method provides
CC   multi-finger zinc finger proteins with improved affinity and specificity
CC   for their target sequences, as well as enhanced biological activity. The
CC   present sequence represents a zinc finger protein DNA target sequence.
XX
SQ   Sequence 9 BP; 2 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTC 24
              ||||||||
Db          2 AGGGAGTC 9


RESULT 484
ADA64129/c
ID   ADA64129 standard; DNA; 9 BP.
XX
AC   ADA64129;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Zinc finger target sequence DNA #587.
XX
KW   ds; target sequence; zinc finger protein;
KW   multi-finger zinc finger protein; improved affinity;
KW   improved specificity; enhanced biological activity.
XX
OS   Synthetic.
XX
PN   US2003068675-A1.
XX
PD   10-APR-2003.
XX
PF   20-NOV-2001; 2001US-00990186.
XX
PR   24-MAR-1999;   99US-0126238P.
PR   24-MAR-1999;   99US-0126239P.
PR   30-JUL-1999;   99US-0146595P.
PR   30-JUL-1999;   99US-0146615P.
PR   23-MAR-2000; 2000US-00535008.
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (LIUQ/) LIU Q.
XX
PI   Liu Q;
XX
DR   WPI; 2003-567233/53.
XX
PT   Designing zinc finger protein that has three zinc fingers from N-terminus
```

```
PT   and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT   site, by selecting zinc fingers that bind their respective subsites.
XX
PS   Disclosure; Page 22; 34pp; English.
XX
CC   The invention relates to a method of designing a zinc finger protein. The
CC   method is useful for designing a zinc finger protein. The method provides
CC   multi-finger zinc finger proteins with improved affinity and specificity
CC   for their target sequences, as well as enhanced biological activity. The
CC   present sequence represents a zinc finger protein DNA target sequence.
XX
SQ   Sequence 9 BP; 2 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCCTACGT 12
              ||||||||
Db          9 CCCTACGT 2


RESULT 485
ADA64127/c
ID   ADA64127 standard; DNA; 9 BP.
XX
AC   ADA64127;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Zinc finger target sequence DNA #585.
XX
KW   ds; target sequence; zinc finger protein;
KW   multi-finger zinc finger protein; improved affinity;
KW   improved specificity; enhanced biological activity.
XX
OS   Synthetic.
XX
PN   US2003068675-A1.
XX
PD   10-APR-2003.
XX
PF   20-NOV-2001; 2001US-00990186.
XX
PR   24-MAR-1999;   99US-0126238P.
PR   24-MAR-1999;   99US-0126239P.
PR   30-JUL-1999;   99US-0146595P.
PR   30-JUL-1999;   99US-0146615P.
PR   23-MAR-2000; 2000US-00535008.
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (LIUQ/) LIU Q.
XX
PI   Liu Q;
XX
DR   WPI; 2003-567233/53.
XX
PT   Designing zinc finger protein that has three zinc fingers from N-terminus
PT   and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT   site, by selecting zinc fingers that bind their respective subsites.
XX
PS   Disclosure; Page 22; 34pp; English.
XX
CC   The invention relates to a method of designing a zinc finger protein. The
CC   method is useful for designing a zinc finger protein. The method provides
CC   multi-finger zinc finger proteins with improved affinity and specificity
CC   for their target sequences, as well as enhanced biological activity. The
CC   present sequence represents a zinc finger protein DNA target sequence.
XX
SQ   Sequence 9 BP; 2 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCCTACGT 12
              ||||||||
Db          9 CCCTACGT 2


RESULT 486
ADA64482/c
ID   ADA64482 standard; DNA; 9 BP.
XX
AC   ADA64482;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Zinc finger target sequence DNA #940.
XX
KW   ds; target sequence; zinc finger protein;
KW   multi-finger zinc finger protein; improved affinity;
KW   improved specificity; enhanced biological activity.
XX
OS   Synthetic.
XX
PN   US2003068675-A1.
XX
PD   10-APR-2003.
XX
PF   20-NOV-2001; 2001US-00990186.
XX
PR   24-MAR-1999;   99US-0126238P.
PR   24-MAR-1999;   99US-0126239P.
PR   30-JUL-1999;   99US-0146595P.
PR   30-JUL-1999;   99US-0146615P.
PR   23-MAR-2000; 2000US-00535008.
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (LIUQ/) LIU Q.
XX
PI   Liu Q;
XX
DR   WPI; 2003-567233/53.
XX
PT   Designing zinc finger protein that has three zinc fingers from N-terminus
PT   and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT   site, by selecting zinc fingers that bind their respective subsites.
XX
PS   Disclosure; Page 27; 34pp; English.
XX
CC   The invention relates to a method of designing a zinc finger protein. The
CC   method is useful for designing a zinc finger protein. The method provides
CC   multi-finger zinc finger proteins with improved affinity and specificity
CC   for their target sequences, as well as enhanced biological activity. The
CC   present sequence represents a zinc finger protein DNA target sequence.
XX
SQ   Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          9 CGGGCCCT 2


RESULT 487
ADA64483/c
ID   ADA64483 standard; DNA; 9 BP.
XX
AC   ADA64483;
XX
DT   20-NOV-2003  (first entry)
XX
```

```
DE   Zinc finger target sequence DNA #941.
XX
KW   ds; target sequence; zinc finger protein;
KW   multi-finger zinc finger protein; improved affinity;
KW   improved specificity; enhanced biological activity.
XX
OS   Synthetic.
XX
PN   US2003068675-A1.
XX
PD   10-APR-2003.
XX
PF   20-NOV-2001; 2001US-00990186.
XX
PR   24-MAR-1999;   99US-0126238P.
PR   24-MAR-1999;   99US-0126239P.
PR   30-JUL-1999;   99US-0146595P.
PR   30-JUL-1999;   99US-0146615P.
PR   23-MAR-2000; 2000US-00535008.
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (LIUQ/) LIU Q.
XX
PI   Liu Q;
XX
DR   WPI; 2003-567233/53.
XX
PT   Designing zinc finger protein that has three zinc fingers from N-terminus
PT   and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT   site, by selecting zinc fingers that bind their respective subsites.
XX
PS   Disclosure; Page 27; 34pp; English.
XX
CC   The invention relates to a method of designing a zinc finger protein. The
CC   method is useful for designing a zinc finger protein. The method provides
CC   multi-finger zinc finger proteins with improved affinity and specificity
CC   for their target sequences, as well as enhanced biological activity. The
CC   present sequence represents a zinc finger protein DNA target sequence.
XX
SQ   Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          9 CGGGCCCT 2


RESULT 488
AAV50253
ID   AAV50253 standard; DNA; 10 BP.
XX
AC   AAV50253;
XX
DT   21-OCT-1998  (first entry)
XX
DE   Yeast tag for additional NORF chromosome 4 tag position 93873.
XX
KW   Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;
KW   eukaryotic cell; antifungal; SAGE tag; gene expression;
KW   serial analysis of gene expression; probe; ss.
XX
OS   Saccharomyces cerevisiae.
OS   Synthetic.
XX
PN   WO9832847-A2.
XX
PD   30-JUL-1998.
XX
PF   22-JAN-1998;   98WO-US001216.
XX
PR   23-JAN-1997;   97US-0035917P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1998-427943/36.
XX
PT   Yeast transcriptome - useful for modulating eukaryotic cell, for
PT   screening antifungal agents, and for identifying genes in cell cycle
PT   progression.
XX
PS   Claim 1; Page 26; 44pp; English.
XX
CC   Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene
CC   involved in cell cycle progression selected from the group of
CC   nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)
CC   tags for highly expressed genes and NORF genes are given in AAV50051 to
CC   AAV50345. The present invention describes: (1) a method of using yeast
CC   genes to modulate the cell cycle which comprises administering to a cell
CC   an isolated DNA molecule comprising a yeast gene which is involved in
CC   cell cycle progression selected from differentially expressed genes (SAGE
CC   tags given in AAV50051 to AAV50345); (2) a method for screening candidate
CC   antifungal drugs which comprises contacting a test substance with a yeast
CC   cell and monitoring expression of a yeast gene which is involved in cell
CC   cycle progression; (3) a method of identifying human genes which are
CC   involved in cell cycle progression which comprises hybridizing a probe
CC   comprising at least 10 contiguous nucleotides of a yeast gene which is
CC   differentially expressed between at least 2 phases selected from the log
CC   phase, the S phase and the G2/M phase; and (4) a probe for ascertaining
CC   the phase in the cell cycle, where the probe comprises at least 14
CC   contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to
CC   AAV50345), or as an array of probes on a solid support
XX
SQ   Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 GTACAGGG 20
              ||||||||
Db          1 GTACAGGG 8


RESULT 489
AAZ79208
ID   AAZ79208 standard; DNA; 10 BP.
XX
AC   AAZ79208;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1636.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
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PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 112; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CGGGCCCT 8
              ||||||||
Db          3 CGGGCCCT 10


RESULT 490
AAZ77621
ID   AAZ77621 standard; DNA; 10 BP.
XX
AC   AAZ77621;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:49.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
```

```
PS   Claim 1; Page 64; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 CCTACGTG 13
              ||||||||
Db          2 CCTACGTG 9


RESULT 491
AAZ82875
ID   AAZ82875 standard; DNA; 10 BP.
XX
AC   AAZ82875;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2109.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 116; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GGAGTCCA 26
              ||||||||
Db          2 GGAGTCCA 9


RESULT 492
AAZ83886
ID   AAZ83886 standard; DNA; 10 BP.
XX
AC   AAZ83886;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #3120.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
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PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 142; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TGTACAGG 19
              ||||||||
Db          2 TGTACAGG 9


RESULT 493
AAZ82564/c
ID   AAZ82564 standard; DNA; 10 BP.
XX
AC   AAZ82564;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1798.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 107; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GTGTACAG 18
              ||||||||
Db          9 GTGTACAG 2


RESULT 494
AAZ82943/c
ID   AAZ82943 standard; DNA; 10 BP.
XX
AC   AAZ82943;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2177.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
```

```
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 118; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GAGTCCAG 27
              ||||||||
Db          9 GAGTCCAG 2


RESULT 495
AAZ86367
ID   AAZ86367 standard; DNA; 10 BP.
XX
AC   AAZ86367;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #5601.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 206; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GCCCTACG 11
              ||||||||
Db          2 GCCCTACG 9


RESULT 496
AAZ79758/c
ID   AAZ79758 standard; DNA; 10 BP.
XX
AC   AAZ79758;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human breast tumour downregulated gene SAGE tag, SEQ ID NO:49.
XX
KW   SAGE tag; serial analysis of gene expression; diagnosis;
KW   differential gene expression; characterisation; targetted expression;
KW   tumour; cancer; immunotherapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO9966303-A2.
```

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XX
PD   23-DEC-1999.
XX
PF   17-JUN-1999;   99WO-US013820.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106132/09.
XX
PT   New polynucleotide useful in cancer immunotherapy.
XX
PS   Claim 1; Page 54; 97pp; English.
XX
CC   Sequences AAZ79710-Z79916 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts which are
CC   differentially expressed in a variety of normal or malignant cell types.
CC   Some of the transcripts correspond to known genes or ESTs (expressed
CC   sequence tags) which were previously unknown to be preferentially or
CC   differentially expressed in that particular cell type, while other
CC   transcripts correspond to novel genes. The invention also provides a
CC   nucleotide comprising a promoter sequence derived from one of the
CC   differentially expressed genes, which may optionally be operably linked
CC   to a foreign nucleotide sequence, and gene delivery vehicles and host
CC   cells comprising the polynucleotides of the invention. A nucleotide
CC   comprising sequences AAZ79710-Z79916 may be used in diagnostic procedures
CC   to characterise a cell of a specific tissue type and to determine whether
CC   it is normal or malignant. They may be used to screen for agents that
CC   modulate expression of differentially expressed genes compound. The
CC   promoter/foreign gene construct of the invention may be used for
CC   targetted expression of the foreign gene in a particular cell type. For
CC   example, a promoter derived from a gene preferentially expressed in
CC   dendritic cells (antigen-presenting cells, or APCs), may be operably
CC   linked to a sequence encoding an immunostimulatory molecule and a
CC   sequence encoding an antigen. Such a construct could be transduced into
CC   APCs and would be useful for inducing an immune response by educating
CC   immune effector cells in vivo, or in cancer immunotherapy
XX
SQ   Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        12 TGTACAGG 19
             ||||||||
Db         9 TGTACAGG 2


RESULT 497
AAA74368/c
ID   AAA74368 standard; cDNA; 10 BP.
XX
AC   AAA74368;
XX
DT   30-NOV-2000  (first entry)
XX
DE   Mouse transcript tag #4.
XX
KW   Gene expression profile; transcript-specific tag; mouse; ss.
XX
OS   Mus sp.
XX
PN   EP1024201-A1.
XX
PD   02-AUG-2000.
XX
PF   27-JAN-1999;   99EP-00400189.
XX
PR   27-JAN-1999;   99EP-00400189.
XX
PA   (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
PA   (CNRS ) CENT NAT RECH SCI.
XX
PI   Cheval L,  Elalouf J,  Virlon B;
XX
DR   WPI; 2000-500199/45.
XX
PT   Microassay for gene expression analysis in biological material e.g.
PT   specific tissue types, comprises obtaining a library of tags using a
PT   modification of existing SAGE (undefined) technique suitable for small
PT   cell numbers.
XX
PS   Disclosure; Page 4; 35pp; English.
XX
CC   The present invention relates to a method for obtaining a library of
CC   transcript-specific tags. The tags are useful for analysing gene
CC   expression profiles of tissues or cell cultures. Linkers were ligated to
CC   cDNA obtained from two tissue samples: mouse outer medullary collecting
CC   duct and mouse medullary thick ascending limb, via a Sau3A I restriction
CC   site. The resulting products were digested with tagging enzyme BsmF I, to
CC   release the transcript-specific tags (linker-cDNA complex). The present
CC   sequence is an example of a tag generated by the method of the present
CC   invention
XX
SQ   Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 AGGGAGTC 24
              ||||||||
Db          9 AGGGAGTC 2


RESULT 498
AAF99919
ID   AAF99919 standard; DNA; 10 BP.
XX
AC   AAF99919;
XX
DT   12-JUN-2001  (first entry)
```

```
XX
DE   Immunostimulatory nucleic acid #1035.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Disclosure; Page 9; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 ACGTGTAC 16
              ||||||||
Db          1 ACGTGTAC 8


RESULT 499
AAH64096/c
ID   AAH64096 standard; cDNA; 10 BP.
XX
AC   AAH64096;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 936.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US031922.
XX
PR   24-NOV-1999;   99US-00448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell type,
PT   such as cancer cell, comprises transcriptomes expressed in particular
PT   cell types.
XX
PS   Claim 13; Page 60; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences AAH63161-
CC   AAH64724 is expressed by the cell. The transcriptomes described in the
CC   invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of the
CC   transcriptomes described in the exemplification of the invention
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GTGTACAG 18
              ||||||||
Db          9 GTGTACAG 2


RESULT 500
AAH63834/c
ID   AAH63834 standard; cDNA; 10 BP.
XX
AC   AAH63834;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 674.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US031922.
XX
PR   24-NOV-1999;   99US-00448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell type,
PT   such as cancer cell, comprises transcriptomes expressed in particular
PT   cell types.
XX
```

```
PS   Claim 13; Page 54; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences AAH63161-
CC   AAH64724 is expressed by the cell. The transcriptomes described in the
CC   invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of the
CC   transcriptomes described in the exemplification of the invention
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match            28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 ACGTGTAC 16
              ||||||||
Db         10 ACGTGTAC 3


RESULT 501
AAH63624/c
ID   AAH63624 standard; cDNA; 10 BP.
XX
AC   AAH63624;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 464.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US031922.
XX
PR   24-NOV-1999;   99US-00448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell type,
PT   such as cancer cell, comprises transcriptomes expressed in particular
PT   cell types.
XX
PS   Claim 13; Page 49; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences AAH63161-
CC   AAH64724 is expressed by the cell. The transcriptomes described in the
CC   invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of the
CC   transcriptomes described in the exemplification of the invention
XX
SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match            28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 AGTCCAGG 28
              ||||||||
Db         10 AGTCCAGG 3


RESULT 502
AAH32824/c
ID   AAH32824 standard; cDNA; 10 BP.
XX
AC   AAH32824;
XX
DT   13-AUG-2001  (first entry)
XX
DE   LPS activated human monocyte expression gene cDNA tag SEQ:197.
XX
KW   Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW   expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001069993-A.
XX
PD   21-MAR-2001.
XX
PF   28-APR-2000; 2000JP-00131079.
XX
PR   08-JUL-1999;   99JP-00195103.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2001-304369/32.
XX
PT   LPS activated human monocyte expression gene group.
XX
PS   Claim 19; Page 35; 52pp; Japanese.
XX
CC   The present invention describes an lipopolysaccharide (LPS) activated
CC   human monocyte expression gene group consisting of the high-ranking 50
CC   genes of the highest expression among the genes expressed by human
CC   monocyte stimulated by LPS in which the cDNA of each gene has the base
CC   sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
CC   CATG-3' nearest to the polyA region. The gene group is useful for the
CC   development of new means for the diagnosis and the treatment of various
CC   human diseases in which human monocyte plays an important role. AAH32628
CC   to AAH32943 represent specifically claimed LPS activated human monocyte
CC   expression gene cDNA tags from the present invention. AAH32944 represents
CC   an LPS activated human monocyte expression gene cDNA sequence encoding
CC   AAB98009, which are given in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match            28.6%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 ACGTGTAC 16
              ||||||||
Db         10 ACGTGTAC 3


RESULT 503
AAH32796
ID   AAH32796 standard; cDNA; 10 BP.
XX
AC   AAH32796;
XX
DT   13-AUG-2001  (first entry)
XX
DE   LPS activated human monocyte expression gene cDNA tag SEQ:169.
XX
KW   Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW   expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS   Homo sapiens.
```

XX
PN JP2001069993-A.
XX
PD 21-MAR-2001.
XX
PF 28-APR-2000; 2000JP-00131079.
XX
PR 08-JUL-1999; 99JP-00195103.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2001-304369/32.
XX
PT LPS activated human monocyte expression gene group.
XX
PS Claim 10; Page 32; 52pp; Japanese.
XX
CC The present invention describes an lipopolysaccharide (LPS) activated
CC human monocyte expression gene group consisting of the high-ranking 50
CC genes of the highest expression among the genes expressed by human
CC monocyte stimulated by LPS in which the cDNA of each gene has the base
CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
CC CATG-3' nearest to the polyA region. The gene group is useful for the
CC development of new means for the diagnosis and the treatment of various
CC human diseases in which human monocyte plays an important role. AAH32628
CC to AAH32943 represent specifically claimed LPS activated human monocyte
CC expression gene cDNA tags from the present invention. AAH32944 represents
CC an LPS activated human monocyte expression gene cDNA sequence encoding
CC AAB98009, which are given in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCTACGTG 13
||||||||
Db 2 CCTACGTG 9

RESULT 504
ABA06035
ID ABA06035 standard; cDNA; 10 BP.
XX
AC ABA06035;
XX
DT 10-JAN-2002 (first entry)
XX
DE Human normal hepatocyte expression gene cDNA, SEQ ID NO: 12.
XX
KW Human; hepatocyte; gene expression; hepatopathy; ss.
XX
OS Homo sapiens.
XX
PN JP2001211883-A.
XX
PD 07-AUG-2001.
XX
PF 31-JAN-2000; 2000JP-00023170.
XX
PR 31-JAN-2000; 2000JP-00023170.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2001-629566/73.
XX
PT Human normal hepatocyte expression gene group.
XX
PS Claim 1; Page 6; 26pp; Japanese.
XX
CC The invention relates to a human normal hepatocyte expression gene group
CC comprising 200 genes in the human normal hepatocyte. The cDNA of each
CC gene comprises one of 200 fully defined nucleotide sequences as given in
CC the specification. The gene group and the cDNAs corresponding to each of
CC the genes in the group are useful in the diagnosis and treatment of human
CC hepatopathy. The present sequence is a cDNA corresponding to a gene
CC expressed by normal human hepatocytes
XX
SQ Sequence 10 BP; 0 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCCT 8
||||||||
Db 3 CGGGCCCT 10

RESULT 505
AAF37857/c
ID AAF37857 standard; DNA; 10 BP.
XX
AC AAF37857;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4596.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 164; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGTGTACA 17
||||||||
Db 10 CGTGTACA 3

RESULT 506
AAF33470
ID AAF33470 standard; DNA; 10 BP.
XX
AC AAF33470;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:209.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Claim 1; Page 26; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GTACAGGG 20
||||||||
Db 1 GTACAGGG 8

RESULT 507
AAF34993
ID AAF34993 standard; DNA; 10 BP.
XX
AC AAF34993;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1732.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 61; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression